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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AC096689
LOCUS
DEFINITION
Oryza sativa chromosome 3 clone OSJNBa0027J18, *** SEQUENCING IN
ACCESSION
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ALIGNMENTS

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TITLE
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Best Local Similarity
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                                                        136236 ACATGAGCGGGAGCCCCTACGGCGCGAACCAGGGGTGGGCGAGCTACCCGGCGCGCCCCG
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                                                                                                 400
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             CCGAGGTGGTGGCGCTGTGGCGGAGGGGGGGGTACTACACCCACGCCAACAACACGT 519
                                                                                                                                             ACCAGGCGCGGCGGCGGTCGGGGTGGCGCCGCTGCGGTGGAGCGGCGACCTGGCGGCGG
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1 29894: contig of 29894 bp in length

29895 29994: gap of unknown length

70109 70208: gap of unknown length

70209 79598: contig of 9390 pin length

70209 79598: contig of 9390 pin length

70599 79698: gap of unknown length

70699 106423: contig of 26725 bp in length

106424 106523: gap of unknown length

106524 139726: gap of unknown length

139627 139726: gap of unknown length

139627 139726: gap of unknown length

139627 139726: gap of unknown length
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On Jan 9, 2002 this sequence version replaced gi:17530731.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 6 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced
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32302 c 32466 g 40767
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/db_xref="taxon:4530"
/chromosome="3"
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                                                                                                                                                                                                                                                                                                 Direct Submission

Direct Submission

Submitted (04-JUN-2002) The Institute for Genomic Research, 97

Medical Center Dr. Rockville, MD 20850, USA
On Jun 4, 2002 this sequence version replaced gi:20153306.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 17 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Oryza sativa chromosome 3 clone OsopROGRESS ***, 17 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Gryzeae; Oryza.

1 (bases 1 to 450928)

Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Tallon,L., Gansberger,K., Kim,M., Overton II,L., Bera,J., Tsitrin,T., Krol,M., Jarrahi,B., Jin,S., Koo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S., Utterbach,T., Feldblyum,T., Yang,Q., Haas,B., Suh,B., Peterson,J., Quackenbush,J., White,O., Salzberg,S. and Fraser,C. Oryza sativa ssp. japonica cv. Nipponbare OSJNBa0079G12 BAC genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-NOV-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA
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AC103550.6 GI:21322019
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                             CGCACGGCAACGTGCAGGGCCAGAGCCCCTACT 672
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34725 c 33029 g 40330 t
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
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95662: gap of unknown 1
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131728: gap of unknown 1
131728: contig of 7470
131775: gap of unknown 1
131914: contig of 2139
133914: contig of 2139
133961: gap of unknown 1
141548: contig of 7587
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141548: contig of 7587
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                                                                                                                                                                                                                                                                     76861 CGCTCGGCGGCGCCGCCGCGCGCGCGCGGCGGCTGCTGCAGATCAGCGA-GGCGCAG 76803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, rel:81-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contlys. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced by the finished sequence.
                                                                                                                                                                                                          TGCGCGTTCGCGGACGTGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGGGCGAGCTAC 446
                                                                                                                                                                               CAGTTCGTGGTGCCGCAGACGCACCTCCGCGCGATCTACGGCCTGCACCCGCTCAAGTGG 76743
                                                                                                                 AACGCGGGCCTGGCTTCGGCGGCCGCGGGGGACGGTGGCGCAGCAGCGGCGGCAGGGCGGG 386
                                                                                   AGCAGCGACCTGGCGACCTGGCGACGGGTGGGCGGACCAGTACAAGGGCGACTGCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki,T., Matsumoto,T. and Yamamoto, Oryza sativa nipponbare(GA3) genomic clone:0J1316_E06
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Eukaryota; Viridiplantae; Streptophyta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki, T., Matsumoto, \bar{T}. and Yamamoto, K. Direct Submission
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                                                                                                  AL Submitted (18-JUL-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced by the finished sequence as soon as it is the accession number will be preserved.

* This sequence will be replaced to the finished sequence.
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Oryza sativa (japonica cultivar-group) oryza sativa (japonica cultivar-group) Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaa.
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2 (bases 1 to 153428)
2 Sasaki, T., Matsumoto, T. and Katayose, Y.
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                                                                                                                                                                                                                              /clone="OSJNBa0054K20"
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/chromosome="2"
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/cultivar="Nipponbare"
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Zea mays
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                                                                                                                                                                                                                                                                                               Morris, S.W.,
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/gene="Pr-1"
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/codon_start=1
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QYYDHDTNSCAEGQVCGHYTQVVWRDSTAIGCARVVCDNNAGVFIICSYNPPGNVVGE
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/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (05-JUL-2001) Takuji Sasaki, National Institute of Agrobiological Siences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-39-7441, Fax:81-298-38-7468)

On Nov 12, 2001 this sequence version replaced gi.15718430. Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTW2.0, BLASTV2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, in the CDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTW2.0. ESTS represent the identified cDNA sequences using RIASTW 2.0. in the coding regions were searched against NCBI NonRedundant Protein database with BLASTW2.0.
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Eukaryota; Viridiplantae; Streptophyta; E
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                            Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic Doclone:OSJNBa0091E23
                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:OSJNBa0091E23.
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                                                                                                                                                                                                                                          Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission
                                                                                                                                                                                                                                                                          Published Only in Database (2001) 2 (bases 1 to 155939)
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```

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corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from -21M13 to M13rev of the BAC clone. Detailed information on overlap and assembly quality together with annotation of this entry is available at
```

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/gene="OSJNBa0091E23.6"
join(29342. .29466,29780.
/gene="OSJNBa0091E23.6"
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GCSDAAVRGGDFFLTRVDANAGWRVQDCRHGRLLFANESDLLVYDPLSRRGVSIRRPS
                                  /translation="mrrgrkrkragkpTCLpPaDaSfPSIDSLNDDVLEEILVRLPCI
aSLaraaCaCarlraIaSSWafLrrfRTLHPSLLGHFATDADDESVIPTfHParaQfD
                                                                                                                                                                          /product="similar
P0455H0310.25"
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                                                         AP004057
AP004057.1 GI:15208425
HTG: HTGS_PHASE2.
Oryza sativa (japonica cultivar-group)
Clone:JJ1316_E06.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magonliophyta; Illiopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                    AP004057 110235 bp DNA Oryza sativa (japonica cultivar-group) 031316_E06, *** SEQUENCING IN PROGRESS
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/gene="OSJNBA0091E23.11"
/codon_start=1
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OSJNBA0077G22.24"
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join(46301. .46382,47219. .4
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SLLSLRHRHPDQAHS
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VINÞKRÞSEYSYFÞGMQAAGRIYWKHRDTTKLQVFDAGÞMRFSYVHLÞEGVHÞRSKYA
VGEAEDGGCCLVVLADAÞHGTVFKVWRLRTGKGSWÞWAWTWELERRLÞACEVIGKVQY
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/db_xref="GI:18461281"
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EIDRVYGGSRRHDDDDVGDDVTTGGGSSLQTRRRTTARREERRAPARRGERGELTGDQ
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<sup>7</sup>3,53518. .53613,53723. .537
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The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be preserved.

* This sequence will be preserved.
                                                                                                                                                                                                   GAGCTACCGCGCGCGCCGAGGTGGTGGCGCTGTGGGTGGCGGAGGGGCGGTACTA
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GTGGCGCGGCACCACCTCCGTCGGCTGCGCCCGCGTCGCCTGCGACGACGACGGCGTCTT 75449
                                                                                     CTCGTACGCCGAACGCGTGCGCGGGCGGGCGAGTGCGGCCACTACACCCAGATCGT
                                                                                                                           CACCCACGCCAACAACACGTGCGCCGCGGGGGGGGGAGTGCGGCACGTACACGCAGGTGGT
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                                          GTGGCGCAACACCGCCGAGGTCGGGTGCGCGCCAGGCCAGGCTGCGCCACGGCCACGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 110235)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
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23562 c 24043 g
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="2"
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Pred. No. 1.6e-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of l contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* This sequence will be replaced
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                                               CATGTCCGTGGCGAAGTGCGCCGGGTGCGCCGCTGGGCGCGTGGGCCGAGTCCCTGGA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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HTG; HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki,T., Matsumoto,T. and Katayose,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Only in Data 2 (bases 1 to 153428)
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43229 a 34064 c 34273 g 41801
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    -- CCGCACAACCAGGCGCGCGCGGCGGTGGGCGTGGCCCCGCTGCGGTGGAA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa/cultivar="Nipponbare"/db_xref="taxon:39947"
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Pred. No. 1.2e-06;
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Oryza sativa (japonica cultivar-group)
Dryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 151673)
Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Kim, M.M., Overton II, L.L., Bera, J.J., Tsitrin, T., Krol, M.I., Jarrahi, B.B., Jin, S.S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S.S., Utterback, T.T., Feldblyum, T.V., Yang, Q.Q., Haas, B.J., Suh, B.B., Deterson, J.J., Quackenbush, J., White, O., Salzberg, S.L. and Erzer, C.M., J., Quackenbush, J., White, O., Salzberg, S.L. and
                                                                         Submitted (08-AUG-2002) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, rbuelletigr.org on Aug 6, 2002 this sequence version replaced gi:19881800.
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BAC clone OSJNBa0040E17 is from Oryza sativa chromosome 10 The orientation of the sequence is from SP6 to T7 end of the
                                                                                                                                                                                Submitted (06-AUG-2002) The I Medical Center Dr. Rockville, 5 (bases 1 to 151673)
                                                                                                                                                                                                                                                                   Medical Center Dr, Rockville, MD 20850, USA 4 (bases 1 to 151673)
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Direct Submission
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                                                          Address all correspondence to:rice@tigr.org
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Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), and GeneSpilcer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://genome.wustl.edu/eddy/tRNAscan-SE).
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SOURCE
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nes 270; Conserv
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              2 (bases 1 to 864)
Park,M.-Y., Moon,E. and Hwang,D.-J.
Direct Submission
Submitted (19-SEP-2000) Molecular Genetics, Natic Agricultural Science and Technology, Seodundong, 441-707, Korea
                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaea; Oryza.
1 (bases 1 to 864)
Park,M.-Y., Moon,E. and Hwang,D.-J.
Isolation and characterization of PRI from rice
                                                                                                                                                                                                                                                                                                                                                                                         AF306651 864 bp mRNA linear PLN 01-JUN-
Oryza sativa pathogenesis-related protein 1 mRNA, complete cds.
AF306651
                                                                                                                                                                                                                                                                                                        Oryza sativa
                                                                                                                                                                                                                                                                                                                           Oryza sativa.
                                                                                                                                             Unpublished
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National Institute dong, Suweon, Kyungl

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PLN 01-JUN-2002

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REFERENCE
AUTHORS
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OTYZA SATIVA genomic DNA complete sequence.
AL731633.1 GI:20452131
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Oryza sativa
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
             Han, B., Feng, Q., Huang, Y.C., Li, Y., Zhu, J.J., Zhao, Q., Hu, X., Liu, Y.L., Mu, J., Yu, Z., Chen, L., Fan, D.L., Weng, Q.J., Zhang, L., Lu, Y.Q., Yu, S.L., Liu, X.H., Lu, T.T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y., Hu, H., Jia, P.X., Qian, Y.M., Ying, K., Zhou, B., Chen, Z.H., Hao, P., Zhang, L., Wu, M., Zhang, R.Q., Guan, J.P., Fu, G
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/organism="Oryza sativa"
/cultivar="Hwachung"
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74. 571
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/codon_start=1
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Pred. No. 3.1e-05;
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                                      CAACCCGCACGGCAACGTGCAGGGCCCAGAGCCCCTACTAGCTA
                                                                          GCTCGGCTGCGCGCGCACCTGCCGCAACGGCGTCGACACCGTCGCCGTCTGCGACTA
                                                                                                            GGTCGGGTGCGCGAGGCCAGCTGCGCCACGGG----CGCCACGCTCACGCTCTGCCTGTA 634
                                                                                                                                                                                                                        bhanéncgr.ac.cn
bhanéncgr.ac.cn
cryza sativa japonica (nipponbare) genomic
clone; OSJNBB0096E05
Web site: http://www.ncgr.ac.cn
web site: http://www.ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a complete sequence. Genes were identified by a combination of several methods: Gene prediction programs including Fegenesh (http://www.softberry.com/), genscan (http://ccR-081.mit.edu/GENSCAN.html), GeneMarkHMM (http://genemark.biology.gatech.edu/GeneMark/), tRNAscan-SE (Sean Eddy, http://genome.wusti.edu/eddy/ERNAscan-SE)), searches of the complete sequence against NCBI none redundant protein database (nr) (ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-JUN-2002) Han Bin, National Center Chinese Academy of sciences, 500# Cao Bao Road, CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang,S.Y., Ren,S.X., Lv,G., Lin,W., Gu,W.Q., Zhu,G.F., Tu,Y.F., Jia,J., Yin,H.F., Zhang,Y., Cai,Z., Chen,J., Kang,H., Chen,X.Y., Shao,C.Y., Sun,Y., Hu,Q.P., Zhang,X.L., Zhang,W., Wang,L.J., Ding,C.W., Sheng,H.H., Gu,J.L., Chen,S.T., Ni,L., Zhu,F.H. and
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/clone_125"
/clone_115="CUGI-OSJNBb"
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248; Conservative
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                                                                                                                                                                                                                                                             371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-AUG-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This sequence will be replaced

* the accession number will be preserved.
GGAGAAGGGCTCCTACGACTACGCCAGCAACAGCTGCGTCGGCGGCGCCCATGTGCGGCCA 8280:
                                                                                                     CGCCGGCGACTGCGCTGCGGCACTCCGATCGCAACAACTATCAGTACGGCGAGAACCT 82683
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Cryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae;
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome clone:OJ1212_C12
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/cultivar="Nipponbare"
/db_xref="rtaxon:39947"
/chromosome="7"
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Submitted (01-AUG-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between the are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working daraft' sequence.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working daraft' sequence.
                                         GGCCCCGCTGCGGTGGAACGCGGGCCTGGCTTCGGCGGCGGCGGGGGACGGTGGCGCAGCA 370
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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/chromosome="7"
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/cultivar="Nipponbare"
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                                                                                                                                                                                                   Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakiénias affrc go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced * Yorking draft' sequence.

* This sequence will be replaced * This sequence as soon as it is available and the accession number will be preserved.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Illiopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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2 (bases 1 to 137275)
Sasaki, T., Matsumoto, T. and Katayose, Y.
Direct Submission
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
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RS. Muzny, D. M., Adins, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bulky, C., Burch, P., Burkett, C., Burnell, K. L., Byrd, N. C., Carron, T. F., Carter, M., Cavazos, S.R., Chack, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C. D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Delgado, O., Davy, Carroll, L., Dederich, D.A., David, R., Delgado, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Garcia, A., Ganrer, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hakes, A., Hernandez, J., Harris, K., Hart, M., Havlak, P., Hakes, A., Hernandez, J., Homsi, F., Howard, S., Haber, J., Halyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kartovoic, J., Kureshi, A., Landry, N., Leal, B., Levis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTACACGCAGGTGGTGTGGCGCAACACCGCCGAGGTCGGGTG---CGCGCAGGCCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGGTGGGCGAGCTACCGCGCGCGCGCCCCGAGGTG-----GTGGCGCTGTGGGTGGC
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AC128878.2 GI:22038229
HTG; HTGS_PHASE1.
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Rattus norvegicus clone CH230-511F16,
***, 55 unordered pieces.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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Pred. No. 3.1e-05;
0; Mismatches 181;
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		TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT
	Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu/ Center project name: KAXI Center project name: CH230-511P16 Center clone name: CH230-511P16 Consensus quality: 117283 bases at least Q40 Consensus quality: 117283 bases at least Q20 Consensus quality: 128074 bases at least Q20 **NOTE: Stimated insert size may differ from sequence length ** (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). ** NOTE: This is a "working draft' sequence. It currently ** consists of 55 contigs. The true order of the pieces ** is not known and their order in this sequence record is ** arbitrary. Gaps between the contigs are represented as ** runs of N, but the exact sizes of the gaps are unknown. ** This record will be updated with the finished sequence ** as soon as it is available and the accession number will ** be preserved.	Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Makhiney, E., McLeod, M.P., Meador, M., Mel, G., Melt, G., Melt, G., Miner, G., Miner, G., Miner, G., Miner, G., Miner, C., Mitchell, T., Mohabat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Ngu
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Search completed: March 18, 2003, 15:14:28 Job time: 3824 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23606 GGGGAGGGG 23598
                                                                                                                                                                                                   522 GCCGCGGG 530
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104293: contig of 5272 bp in length
104393: gap of unknown length
108459: contig of 4066 bp in length
108459: contig of 4066 bp in length
113545: contig of 4986 bp in length
113645: gap of unknown length
117970: contig of 4325 bp in length
118070: gap of unknown length
122690: contig of 4620 bp in length
122790: gap of unknown length
127723: gap of unknown length
127723: gap of unknown length
136739: contig of 4833 bp in length
136839: gap of unknown length
142131: contig of 5292 bp in length
142131: gap of unknown length
150886: gap of unknown length
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Perfect score:
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
167	171.5	191.5	197	234	242	242	243	246	249.5	256.5	257	257.5	260	260.5	261.5
15.4	15.8	17.6	18.2	21.6	22.3	22.3	22.4	22.7	23.0	23.6	23.7	23.7	24.0	24.0	24.1
204	81	177	160	162	177	168	161	176	161	210	161	175	177	164	174
2	2	N	ν	N	N	Ν	N	Ν	N	N	Ν	N	N	2	N
S27448	A05264	D84583	D85077	A96537	T08126	T07146	в96537	F84583	T52399	T04233	E85354	S43894	S04728	T04299	S71554
Sc7 protein - brac	pathogenesis-relat	probable pathogene	probable pathogene	hypothetical prote	pathogenesis-relat	pathogenesis-relat	hypothetical prote	pathogenesis-relat	pathogenesis-relat	pathogenesis-relat	PR-1-like protein	pathogenesis-relat	pathogenesis-relat	pathogenesis-relat	pathogenesis-relat

ALIGNMENTS

PA; ABANAMANA ANA ANA ANA ANA ANA ANA ANA ANA	Qy Db	Qy Db	Qy Db	Qy Db	7 m 10
RESULT 2 T02054 T02054 T02054 T02054 Pathogenesis related protein-1 - maize C;Species: Zea mays (maize) C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 11-May-2000 C;Accession: T02054 R;Morris, S.W.; Vernooij, B.; Titatarn, S.; Starrett, M.; Thomas, S.; Wiltse, C.C.; Mol. Plant Microbe Interact. 11, 643-658, 1998 Mol. Plant Microbe Interact. 11, 643-658, 1998 A;Title: Induced resistance responses in maize. A;Reference number: Z14524; MUID:98313983; PMID:9650297 A;Accession: T02054	200 QSPY 203 : 211 EKPY 214	141 AEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATG-ATLTLCLYNPHGNVOG 199 :: : : : : : : : :	82 GVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYR-ARPAEVVALWV 140 	22 LILATILALCAAPAPTHGARVIMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV 81	Query Match 32.9%; Score 357.5; DB 2; Length 214; Best Local Similarity 41.3%; Pred. No. 7.8e-22; Matches 76; Conservative 26; Mismatches 75; Indels 7; Gaps

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pathogenesis-related protein 1 - maize
C;Species: Zea mays (maize)
C;Date: 08-Mar-1991 #sequence_revision 08-Mar-1991
C;Accession: A33155
R;Gillikin, J; Burkhart, W; Graham, J.S.
submitted to the Protein Sequence Database, Februar
A;Reference number: A33155
A;Accession: A33155
A;Accession: A33155
A;Rolecule type: protein
A;Residues: 1-140 <GIL>
C;Superfamily: pathogenesis-related leaf protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-163 <MOR>
A; Cross-references: EMBL:U82200; NID:g3290003; PIDN:AAC25629.1; PID:g3290004
C; Genetics:
A; Gene: PR-1
C; Superfamily: pathogenesis-related leaf protein
                                                                                                                                                                        RESULT 4
S37166
submitted to the EMBL Data Library, A;Description: Purification characte A;Reference number: S37186 A;Accession: S37166 A;Status: preliminary
                                                                                pathogenesis-related protein la - barley
N;Alternate names: pathogenesis-related protein Hv-la
C;Species: Hordeum vulgare (barley)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C;Accession: S37166
R;Bryngelsson, T.; Sommer-Knudsen, J.; Gregersen, P.L.; Collinge, D.B.; Ek,
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                                                                                                                                                                                                                                       FIICSYNPPGNVVGESPY 140
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                                                                                   Sommer-Knudsen, J.; Gregersen, P.L.; Collinge, D.B.; Ek, B.;
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                                                         characterization
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1; Mismatches
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A; Molecule type: mRNA A; Residues: 1-164 <BRY> A; Residues: 1-164 <BRY> A; Cross-references: EMBL: X74939; NID: 9401830; PIDN: CAA52893.1; C; Superfamily: pathogenesis-related leaf protein
pathogenesis-related protein - maize C;Species: Zea mays (maize) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text C;Accession: S14969 R;Casacuberta, J.M.; Puigdomenech, P.; San Segundo, B. Plant Mol. Biol. 16, 527-536, 1991 Plant Mol. Biol. 16, 527-536, 1991 A;Title: A gene coding for a basic pathogenesis-related A;Reference number: S14969; MUID:91329688; PMID:1714315 A;Accession: S14969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathogenesis-related protein T16L1.220 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: T16L1.220
C; Superfamily: pathogenesis - related leaf protein
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A; Residues: 1-172 <BEV>
A; Cross-references: EMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: cultivar Columbia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 LATILIALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                             GATLTLCLYNPHGNVQGQSPY
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                                                                                                                                                                                                                                                                                                                                                                                       LAFGSGDMSAAQAVAMWVHEKSYYDFYSNSC-HGPACGHYTQVVWRGSARLGCGKAKCNN
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Pred. No. 5.5e
19; Mismatches
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Pred. No. 6.9
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ies 56;
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A; LIUSS-TETERENCES: EMBL:X03465; NID:g19977; PIDN:CAA27183.1; PID:g456200
A; Experimental source: Nicotiana tabacum cv. Samsun NN after inoculation w R; Ohshima, M.; Harada, N.; Matsuoka, M.; Chashi, Y.
Nucleic Acids Res. 18, 181, 1990
A; Title: The nucleotide sequence of pathogenesis-related (PR) 1b protein g A; Reference number: S07579; MUID:90174914; PMID:2308824
A; Accession: S07579
A; Status: translation not shown
A; Molecule tvoe· Nuna
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A:Molecule type: DNA
A;Residuse: 1-167 <CAS>
A;Cross-references: EMBL:X54325; NID:g22453; PIDN:CAA38223.1;
C;Superfamily: pathogenesis-related leaf protein
A; Cross references: EMBL: M12486; NID:g19947; PIDN:CAA31009.1; PID:g19948 A; Cross references: EMBL: M12486; NID:g19947; PIDN:CAA31009.1; PID:g19948 A; Pipme, G; Parks, T.D.; Burkhart, W.; Dincher, S.; Ahl, P.; Metraux, J.1 Plant M01. Biol. 11, 89-94, 1988 A; Title: Isolation of the genomic clone for pathogenesis-related protein : A; Reference number: $04032 A; Recession: $06858 A; Molecule type: protein A; Residues: 94-110; M18-153; M18-168 < PAY> C; Superfamily: pathogenesis-related leaf protein C; Keywords: pyroglutamic acid F; 1-30/Domain: Signal sequence #status predicted <SIG> F; 31-108/Product: pathogenesis-related protein 1b #status predicted <MAT> F; 31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathogenesis-related protein 1b precursor - common tobacco (;Species: Nicotiana tabacum (common tobacco) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 2 c;Accession: B24620; S07579; S02223; S06858 R;Cornelissen, B.J.C.; Hooft van Huijsduijnen, R.A.M.; Van Loon, EMBO J. 5, 37-40, 1986 EMBO J. 5, 37-40, 1986 A;Title: Molecular characterization of messenger RNAs for 'pathog A;Reference number: A24620
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                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Isolation and nucleotide sequence of cDNA clones A; Reference number: S01705; MUID:89041576; PMID:3186451 A; Accession: S02223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-168 <COR>
A; Cross references: EMBL: X03465;
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A; Residues: 1-168 <OHS>
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J.P.; Klessig, D.F.
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Metraux, J.P.;
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A; Residues: 1-179 < EYA>
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Plant Mol. Biol. 19, 589-59, 1992
A;Title: Dark induced accumulation of a basic pathogenesis-related A;Reference number: S22531; MUID:92329719; PMID:1627772
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A; Residues: 1-184 <PFI>
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                                                                                                                           A; Cross-references:
                                                                                                                                                                               A; Accession: S22531
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                                                                      Superfamily:
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Best Local
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Best Local
                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                  146
                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
Local Similarity 43.4 es 62; Conservative
                                                                                      prb-1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQYGENLAQGSGDFMT-AAKAVEMMVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQGWASYR-ARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAQASCATGATLTLCLXNPHGNVQGQSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPYGAN - - QGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA---- 116
                                                                                                                                                                                                                                                                                                                                                                                                                  NSGGYVVSCNYDPPGNFVGQSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGATLTLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAQNSPQDYLDAHNTARADVGVEPLTWDDQVAAYAQNYASQ--LAADCMLVH-SHGQYGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHAQNSQQDYLDAHNTARADVGVEPLTWDNGVAAYAQNYVSQ-----LAADCNLVHSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLAWGSGDFMTAAKAVEMWVNEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARAQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                      pathogenesis-related leaf protein
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                                                                                                                           EMBL: X66942;
                 27.9%;
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                                                                                                                         NID: g19969;
                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 304; DB 2;
Pred. No. 1.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 304; DB 2;
Pred. No. 1.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                    168
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7; Mismatches
                     Score 302.5;
Pred. No. 1.
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                                                                                                                             PIDN:CAA47374.1;
                   8e-17
                                     DВ
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                                   Length
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                                     179;
                                                                                                                           PID:g19970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:g20056
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Matches

17;

Mismatches

61;

Indels

Ψ

Gaps

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pathogenesis-related protein 1c precursor - common tobacco C; Species: Nicotiana tabacum (common tobacco C; Species: Nicotiana tabacum (common tobacco) C; Date: 30 - Jun-1988 #sequence_revision 01-Dec-1995 #text_ch C; Accession: S07580; C24620; S01705 R; Ohshima, M.; Harada, N.; Matsuoka, M.; Ohashi, Y. Nucleic Acids Res. 18, 182, 1990 A; Title: The nucleotide sequence of pathogenesis-related (FA; Reference number: S07580; MUID:90174915; PMID:2308825 A; Accession: S07580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position:
A; Note: T16L1.21
C; Superfamily: p:
F; 1-26/Domain: s
F; 27-163/Product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
T04989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathogenesis-related protein 1 precursor, 19.3K - Arabidopsis thaliana N;Alternate names: protein T16L1.210 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000 C;Accession: T04989; S71271 R;Beyan, M.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-77,'p',79-82,'L',84-88,'RL',91-92,'RR',95-162,'LLKENSI'
A; Cross-references: EMBL:X96600; NID:g1228948; PID:g1228950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Kloska, S.; Schuster, W. submitted to the EMBL Data Library, A;Reference number: S71271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: cultivar Columbia; BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-163 <BEV>
A; Cross-references: EMBL: AL031394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z15393
A; Accession: T04989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the Protein
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Superfamily: pathogenesis-related leaf protein
;1-26/Domain: signal sequence #status predicted <SIG>
;27-163/Product: pathogenesis-related protein 1, 19.3K #status predicted
                                                                                                                                                                                                                                                                                                                189
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                                                                                                                                                                                                                                                                                                                CLYNPHGNVQGQSPY
                                                                                                                                                                                                                                                                                                                                                  NNGWYFITCNYDPPGNWRGQRPY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANQCWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASC
                                                                                                                                                                                                                                                                              CNYDPPGNWVGEWPY
                                                                                                                                                                                                                                                                                                                                                                                                                          DFLAVHNRARAEVGVGPLRWDEKVAAYARNYANQ--RKGDCAMKHSSGS-YGENIAWSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
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45.28;
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                                                                                                                                                                                                                                                                              163
                                                                                                                                                                                                                                                                                                                203
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Pred. No. 4.2
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, November 1998
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                                                                                                                                               #text_change
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A;ACCESSION.
A;Rolecule type: DNA
A;Residues: 1-166 <KLO>
A;Cross-references: EMBL:X96600; NID:g1228948; PIDN:CAA65419.1; PID:g1228949
A;Cross-references: EMBL:X96600; PID:g12289499
A;Cross-references: EMBL:X96600; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogenesis-related protein 1 precursor, 18.9K - IN INTERPRETARION PROTEIN THE PROPERTY OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Kloska, S.; Schuster, W. submitted to the EMBL Data A;Reference number: S71270 A;Accession: S71270
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A;Note: T16L1.200
C;Superfamily: pathogenesis-related leaf protein F;1-27/Domain: signal seguence #status predicted F;28-166/Product: pathogenesis-related protein 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-166 <BEV>
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R;Cutt, J.R.; Dixon, D.C.; Carr,
Nucleic Acids Res. 16, 9861, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-168 <OHS>
A; Cross-references: EMBL:X17681;
R; Cornelissen, B.J.C.; Hooft van
EMBO J. 5, 37-40, 1986
                                                                                                                                                                                                                                   A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the Protein Sequence Database, A; Reference number: Z15393
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A; Residues: 6-168 <CUT>
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A; Accession: C24620
                                                                                                                                                                                                                                                                                                  A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: cultivar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T04988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library, March 1996
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pathogenesis-related protein 1 precursor - barley C.Species: Hordeum vulgare (barley) C.Species: Hordeum vulgare (barley) C.Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change C.Accession: S39474; S32002 R.Muradov, A.; Petrasovits, L.; Davidson, A.; Scott, K.J. Plant MOI. Biol. 23, 439-442, 1993 A.;Title: A cDNA clone for a pathogenesis-related protein 1 from A.Reference number: S39474; MUID:94033324; PMID:8219079 A.; Mccession: S39474 MUID:94033324; PMID:8219079 A.; Mccession: S39474 A.; Molecule type: mRNA A.; Molecule type: mRNA A.; Molecules: 1-164 <MURD: MOID: 
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C:Species: Hordeum vulgare (barley)
C:Date: 14-7ul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Aug-1999
C:Accession: S52627; S37188
R;Mouradov, A.; Mouradova, E.; Scott, K.J.
Plant Mol. Biol. 26, 503-507, 1994
A:Title: Gene family encoding basic pathogenesis-related 1 proteins in barle
A:Reference number: S52626; MUID:95036024; PMID:7524728
A;Rocession: S52627
A;Molecule type: mRNA
A;Residues: 1-164 -MOUD
A;Residues: 1-164 -MOUD
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mes 72; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVALWVA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKKDYNYGSNTCAAGKVCGHYTQVVWRASTSIGCARVVCNNNRGVFIT-CNYEPRGNIVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT - - GATLTLCLYNPHGNVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAILLALAMAAAMVN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHARDDVSVPHIKWHAG-AARYAWNYAQRRKRDCRLIHSNSRGRYGENLAWSSGDMSGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRARPAE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
EMBL: Z21494; NID: g22760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.8%;
39.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 290.5;
Pred. No. 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LSQAQN-----SPQDYVSPHNAARSAVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 8.2e-17;
72;
PIDN:CAA79703.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164;
PID: g22761
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                                                                                                                                                       barley
                                                                                                                                                                                                                                                                                 20-Aug-1999
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; pMID:10617197

A;Accession: C84519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathogenesis-related protein 1 precursor, 17.6K - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 30-Sep-1993 *sequence_revision 30-Sep-1993 *text_change 16-Feb-2001 C:Accession: JQ1693; pQ0471; C84519 C:Accession: JQ1693; pQ0471; C84519 R;Uknes, S.; Mauch_Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch_Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch_Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch_Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch_Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch_Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mani, 
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JQ1693
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A;Accession: PQ0471
A;Molecule type: protein
A;Residues: 42-67;104-112;153-161 <UKN1>
A;Experimental source: leaf
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Дb
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                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: pathogenesis-related leaf protein F;1-26/Domain: signal sequence #status predicted · F;27-161/Product: pathogenesis-related protein 1,
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A; Title: Acquired resistance in Arabidopsis
A; Reference number: JQ1693; MUID:93005717;
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A; Residues: 1-161 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: At2g14610
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A; Residues: 1-161 <UKN>
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                                                                                                                                                                         EQLR-GNCRLIHSG-GPYGENLAWGSGDLSGVSAVNMWVSEKANYNYAANTC--NGVCGH
                                                              QQRRQGGCAFADVGASPYGANQGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGT 161
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39.5%;
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                                                                                                                                    --SPQDYLRVHNQARGAVGVGPMQWDERVA-AYARSYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NID: g3810599; PIDN: AAC69381.1;
                                                                                                                                                                                                                                                              Score 288; DB 2; Pred. No. 2.4e-16; Score 288; DB 2; Pred. No. 2.4e-16; Score 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 288.5;
Pred. No. 2.3
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     SwissProt_40:*
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SC7_SCHC
SC14_SCHCO
YJH8_YEAST
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p09042 nicotiana t
p35792 hordeum vul
005968 hordeum vul
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01-DEC-1992 (Rel. 2
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                  use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement.
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the Eurc
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. W64A; TISSUE-Seed;
MEDLINE-91329688; PubMed-1714315;
Casacuberta J.M., Puigdomenech P., San Segundo B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRMS
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PROSITE: PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE: PS01010; SCP_AG5_PR1_SC7_2; 1.

PROSITE: PS01010; SCP_AG5_PR1_SC7_2; 1.

PROSITE: PS010010; SCP_AG5_PR1_SC7_2; 1.

PROTECTION: Signal.

POTENTIAL.

1 27 PATHOGENESIS-RELATED PROTEIN PRMS

CHAIN 28 167 PATHOGENESIS-RELATED PROTEIN PRMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ranicoideae; Andropogoneae; NCBI_TaxID=4577;
                                                                  Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1;
SMART; SM00198; SCP; 1.
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Panicoideae; An
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                                                                                                                    InterPro; IPR001283; Allrgn_V5/Tpx1
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                                                                                                                                                                                                                                                                                                             INDUCTION: BY FUNGAL INFECTION IN GERMINATING SE SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMM INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION
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                                                                                                                                                  P04284; 1CFE.
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                                                                                                                                                                                                 s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis related protein 1B precursor (PR-1B).
Micotlana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotlana.
                                                                                                                                                                                   MEDLINE=89041576; PubMed=3186451; Cutt J.R., Dixon D.D., Carr J.P., Klessig D.F.; "Isolation and nucleotide sequence of cDNA clones pathogenesis-related proteins PRLa, PRLb and PRLc tabacum cv. Xanthi nc induced by TMV infection."; Nucleic Acids Res. 16:9861-9861(1988).
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                             proteins to the extracellular space idioblasts."
                                                                    MEDLINE=91224081; PubMed=2026137;
Dixon D.C., Cutt J.R., Klessig D.F.;
"Differential targeting of the tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Samsun NN;
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CC ASTERIACOPY;
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PROSITE; PS01009; SCP_AG5_PR1_SC7_1;
PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
Plant defense; Pathogenesis-related;
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                                                                                                                                                                                                                  01-NOV-1988 (Rel. 09, Created)
01-RPR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis-related protein 1C precursor (PR-1C).
Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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ProDom; PD000542; Allrgn_V5/Tpx1; 1.
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STRAIN-cv. Samsun NN; TISSUE-Leaf; MEDLINE-90174915; PubMed-2308825; Ohshima M., Harada N., Matsuoka M.
                                                                                                                                        Spermatophyta; Magnoliophyta; eudicotyledons; c. Asteridae; euasterids I; Solanales; Solanaceae; NCBI_TaxID=4097;
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SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.

INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER PATHOGEN INFECT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAQASCATGATLTLCLYNPHGNVQGQSPY
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                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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        Matsuoka M.,
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EMBL; X05454; CAA29023.1; -.
EMBL; X2487; CAA31010.1; -.
PIR; S07580; S07580.
HSSP; P04284; ICFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PfAm; PF00188; SCP; 1.
PRINTS; PR00837; V5/TPXLIKE.
PRODOM; P000037; V5/TPXLIKE.
PRODOM; P000038; SCP; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91224081; PubMed=2026137; Dixon D.C., Cutt J.R., Klessig D.F.; "Differential targeting of the tobacco proteins to the extracellular space and idioblasts."; EMBO J. 10:1317-1324(1991).
                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfitzner U.M., Goodman H.M.;
"Isolation and characterization of cDNA clones encoding pathogenesi
related proteins from tobacco mosaic virus infected tobacco plants.
Nucleic Acids Res. 15:4449-4465(1987).
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                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1. PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Samsun
MEDLINE=87231027;
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                                                                                                                                                                                                                                                                                     SEQUENCE
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INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMM INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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                                                                           DYLDAHNTARADVGVEPLTWDDQVAAYAQNYASQ
                                                                                                                              EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGANQG
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168 AA;
                                                                                                                                                                                   Conservative
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18583 MW;
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                                                                                                                                                                                   15;
                                                                                                                                                                                                                                Score 296;
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P35792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS, PRO0837; V5TPXLIKE.
ProDom: PD000542; Allrgn_V5/Tpx1;
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Hordeum vulgare (Barley).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Dales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HORVU
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PIR; S37188; S37188.
HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   barley.";
Plant Mol. Biol. 26:503-507(1994).
Plant Mol. Biol. 26:503-507 THE DEFENSE REACTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouradov A., Mouradova E., Scott K.J.;
"Gene family encoding basic pathogenesis-related 1 proteins barley.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

Plant defense; Pathogenesis-telated protein; Signal; Multigene family.

Plant defense; Pathogenesis-Indianity.

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PATHOGENESIS-RELATED PROTEIN PRB1-2.

PATHOGENESIS-RELATED PROTEIN PRB1-2.

PRROLIDONE CARBOXYLIC ACID
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Pfam; PF00188; SCP; 1.
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                                                                                                                                                                                                         LATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGV
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                                                           GAVSWSTKL-QAFAQNYANQ-RINDCKLQHSG-GPYGENIFWGSAGADWKAADAVNSWVN 101
                                                                                                        APLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVALWVA 141
                                                                                                                                                           LAILLALAMAAAMVN
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                                                                                                                                                                                                                                                                                  Similarity
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113
135
164 AA;
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29, Last sequence up
41, Last annotation
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119
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PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                          Score 290.5;
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                                                                                                                                                           -LSQAQN---
                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                  No.
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                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                          61;
                                                                                                                                                         SPQDYVSPHNAARSAVGV
                                                                                                                                                                                                                                                                                                     Length 164;
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Best Local
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PIR; S39474; S39474.
HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1;
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001283; Allrgn_V5/Tpx1
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z21494; CAA79703.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: PROBABLY INVOLVED AGAINST PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94033324; PubMed=8219079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205968;
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                                                                                                                                   LAILLALAMAAAMVN---
                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                        164 AA;
                                                                                                                                                                                                                                    Conservative
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119
150
17683
                                                                                                                                                                                                                                                            26.6%;
                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                 Pred. No. 3.6
; Mismatches
                                                                                                                                                                                                                                                            Score 288.5;
Pred. No. 3.
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use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/profit to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muradov A., Petrasovits L., Davidson A., Scott K.J.;
"A cDNA clone for a pathogenesis related protein 1 from barley.";
Plant MOL. Biol. 23:439-442(1933)
-1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis-related protein 1 precursor.
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
Plant defense; Pathogenesis-related protein; Signal; Multigene Plant defense; Pathogenesis-related protein; Signal; Multigene SIGNAL 1 24 BY SIMILARITY.
CHAIN 25 164 PATHOGENESIS-RELATED PROTEIN 1.
PATHOGENESIS-RELATED PROTEIN 1.
PROCLIDONE CARBOXYLIC ACID
PROCLIDONE CARBOXYLIC ACID
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GAVSWSTKL-QAFAQNYANQ-RINDCKLQHSG-GPYGENIFWGSAGADWKASDAVNSWVS
                                                           APLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVALWVA 141
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les 60;
                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                               -SPQDYVSPHNAARSAVGV
                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
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                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P33154;
01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis related protein 1 precursor (PR-1)
AT2G14610 OR T6B13.15.
Pfam; PF00,188; SCP; 1.
Pfam; PF00,188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpxl; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Eujli C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Mierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uknes S., Mauch-Mani B., Moyer M., Potter S., Wil
Dincher S., Chandler D., Slusarenko A., Ward E.,
"Acquired resistance in Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-cv. Landsberg erecta; TISS MEDLINE-93005717; PubMed-1392589;
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                                                                                                                                                                                                                                      EMBL; M90508; AAA32863.1; -. EMBL; AC005398; AAC69381.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter J.C.; sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20083487; PubMed=10617197;
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                                                                                                                                           InterPro; IPR001283; Allrgn_V5/Tpx1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: INDUCED BY 2,6-DICHLOROISONICOTINIC ACID (INA) AND SALICYLIC ACID (POSSIBLY AN ENDOGENOUS SIGNAL FOR ACQUIRED RESISTANCE). STRONGLY INDUCED BY PATHOCEN INFECTION.

SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SCL4 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: PARTIALLY RESPONSIBLE FOR ACQUIRED PATHOGEN RESISTANCE. SUBCELLULAR LOCATION: ACCUMULATES IN THE APOPLAST BEFORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECRETION
                                                                                                                                                                             JQ1693; JQ1693.
; P04284; ICFE.
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Best Local S
Matches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIA_TOBAC STANDARD; PRT; 168 AA.

P08299;

P01-AUG-1988 (Rel. 08, Created)

P01-AUG-1988 (Rel. 08, Last sequence update)

P1 15-JUN-2002 (Rel. 41, Last annotation update)

P1 Pathogenesis-related protein 1A precursor (PR-1A).

Nicotiana tabacum (Common tobacco).

SNicotiana tabacum (Common tobacco).

ENERTYOTA; Viridiplantae; Streptophyta; Embryophyta; Traces Spermatophyta; Magnoliophyta; endicotyledons; core eudic Asteridae; euasteridas I; Solanales; Solanaceae; Nicotian (PR-1A).
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PROSITE; PS01010:
Plant defense; SIGNAL 1
CHAIN 27
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STRALMS-CV. Addition.

MEDILINE-890441576; PubMed-3186451;

Cutt J.R., Dixon D.D., Carr J.P., Klessig D.F.;

"Isolation and nucleotide sequence of cDNA clones for the nathogenesis-related proteins PRIA, PRIb and PRIC of Nicol
                                                                                                           STRAIN-cv. Wisconsin 38; Pfitzner U.M., Pfitzner A.J.P., Goodman H.M.; Pfitzner A. Pr. Goodman H.M.; "DNA sequence analysis of a PR-la gene from tobacco: relationship of heat shock and pathogen responses in Mol. Gen. Genet. 211:290-295(1988).
                                                                                                                                                                                                                Ohshima M., Matsuoka M., Yamamoto N., Tanaka Y., Ka
Ozeki Y., Kato A., Harada N., Ohashi Y.;
"Nucleotide sequence of the PR-1 gene of Nicotiana
FEBS Lett. 225:243-246(1987).
                                                                                                                                                                                                                                                            STRAIN-cv. Samsun NN;
MEDLINE-88083595; PubMed=3691804;
Ohshima M., Matsucka M., Yamamoto
Ohshima M., Matsucka M., Yamamoto
                                                                                                                                                                                                                                                                                                                               Nucleic [2]
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MEDLINE=88015528; PubMed=3658669;
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                                                                    STRAIN-CV.
                                                                                 SEQUENCE OF 4-168 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                        "Structure of tobacco from the PR-1 group.";
                                                                                                                                                                                                                                                                                                                                                                                                    Cornelissen B.J.C., Horowitz J., van Kan J.A.L., Goldberg R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                          J.F.
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161 AA;
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27
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Res. 15:6799-6811(1987).
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10; SCP_AG5_PR1_SC7_2; 1.
Signal; Pathogenesis related protein.
1 26 POTENTIAL.
1 7 161 PATHOGENESIS-RELATED PROTEIN 1.
7 27 PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
2 (BY SIMILARITY).
3 117 BY SIMILARITY.
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3 117 BY SIMILARITY.
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39.5%;
                                                                                                                                                                                                                                                                                                                                                                        genes encoding pathogenesis-related proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Mismatches
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                                                                                                                                                                                                                                                                 Tanaka Y., Kano-Murakami Y.,
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.9e-16;
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        of Nicotiana
                                                                                                                                                                                                                                    tabacum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eudicots;
                                                                                                                            molecular plants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tracheophyta;
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PIR; A05264; A05264.

HSSP; P04284; ICFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91224081; PubMed=2026137; Dixon D.C., Cutt J.R., Klessig D.F.; Dixon D.C., Cutt J.R., Klessig D.F.; Differential targeting of the tobacco PR-1 pathogenesis-related proteins to the extracellular space and vacuoles of crystal idioblasts."; EMBO J. 10:1317-1324(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tabacum
Nucleic
                                                                                                                                                                                                                                                                          SMART; SM00198; SCP; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1;
PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                                           PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unfamiliar proteins.";
EMBO J. 4:2745-2749(1985).
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                Plant defense;
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00188; SCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Amino acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 30-70;
  49
                         82
                                                 13
                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: PROBABLY INVOLVED IN THE DEFENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: THREE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELATED RESPONSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDUCTION: SYNTHESIZED DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAINST PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                         LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV
  GVEPLTWDDQVAAYAQNYASQ----
                         GVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV
                                                                                                                                                                                                                                                                                                                                                                                                 X05959; CAA29392.1; -.
X06361; CAA29660.1; -.
X12485; CAA31008.1; -.
X06930; CAA30017.1; -.
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Acids Res.
                                                                                                              Similarity
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153
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168
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1 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nc induced by TMV infection."; 16:9861-9861(1988).
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57
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153
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                                                                                                              26.4%;
36.7%;
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                                                                                                                                                             PATHOGENESIS RELATED PROTEIN 1A.

LF >> VS (IN REF. 4).

D -> S (IN REF. 5).

SQ -> PS (IN REF. 5).

D -> N (IN REF. 3).

S -> T (IN REF. 3).

Y -> W (IN REF. 5).
                                                                                                  22;
                                                                                                            Score 286; 1
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                                                                                                                                                 -> T (IN REF. 3).
-> W (IN REF. 5).
27375217031292E0 CRC64;
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---LAADCNLVHSHGQYGENLAEGSGDFMT-AAKA 100
                                                                                               eq. No. 5.8e-1
Mismatches
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                                                 -AQNSQQ
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                                                                                                                                                                                                                                                             protein; Multigene family; Signal.
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                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFECTION OR OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REACTION OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Henschen
                                                                                                                          Length 168;
                                                                                                Indels
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                                                 -DYLDAHNTARADV
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                                                                                                                                                                                                                                                                                                                                              EMBL; 226321; CAA81230.1; -.
EMBL; 726333; CAA81234.1; -.
EMBL; X74940; CAA52894.1; -.
PIR; S37189; S37189.
PIR; S37189; S37209.
PIR; S37167; S37167.
HSSP; P04284; ICEE.
DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HORVU
                                                                                                                                                                                                                                             Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Purification, characterization, and molecular cloning type pathogenesis related proteins from barley."; mol. Plant Microbe Interact. 7:267-275(1994).
-i- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bryngelsson T., Sommer-Knudsen Ek B., Thordal-Christensen H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Pallas; TISSUE=Leaf; MEDLINE=94281675; PubMed=8012045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Psaknon resistant, and cv. MEDLINE=95036024; PubMed=7524728; Mouradova E., Scott K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pathogenesis-related protein PRB1-3 precursor (PR-1B) (HY-8). Hordeum vulgare (Barley). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-cv. Pallas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     barley."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994
15-JUN-2002
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                                                                                                                                                                        SMART; SM00198; SC
PROSITE; PS01009;
PROSITE; PS01010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Mol. Biol.
                                                                          MOD_RES
                                                                                                                             SIGNAL
                                                                                                                                                   Plant
                                                                                                                                                                                                                                                                                                                        InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Gene family encoding basic pathogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAINST PATHOGENS
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                                                                                                                                                     defense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 41, Last annotation updat
     68
113
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                                                                        09; SCP_AG5_PR1_SC7_1; 1.
10; SCP_AG5_PR1_SC7_2; 1.
Pathogenesis-related protein; Signal; Multigene family.
1 BY SIMILARITY.
1 BY SIMILARITY.
5 164 PATHOGENESIS-RELATED PROTEIN PRB1-3.
5 25 PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                             SCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sommer-Knudsen J.,
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     140
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(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
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PRESCRIPTION OF PRESCRIPTION O
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                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRI_SAMNI STANDARD; PRT; 167 AA.
041359;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis related protein PR-1 type precursor.
Sambucus nigra (European elder).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coupe S.A., Taylor J.E., Roberts J.A.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF
-AGAINST PATHOGENS.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                           CHAIN
                                                                                                                                                                                                                            Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                      EMBL; Z46947; CAA87071.1; -.
HSSP; P04284; 1CFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
                                             SEQUENCE
                                                                                                                                              SIGNAL
                                                                                                                                                                    Plant defense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Abscission zone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAE 134
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                                                                                                                                                                                     PS01009; SCP_AG5_PR1_SC7_1; 1. PS01010; SCP_AG5_PR1_SC7_2; 1.
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164 AA;
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72
117
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                                                          Pathogenesis-related protein; Signal.

1 29 POTENTIAL.

1 10 167 PATHOGENESIS-RELATED PROTEIN PR-1 TYPE.

2 144 BY SIMILARITY.

3 123 BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                             ΑĄ;
                                                                                                                                                                                                                                           Allrgn_V5/Tpx1; 1.
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17697 MW;
                                             18410 MW;
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        26.1%;
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Pred. No. 6.2e-16;
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      Score 283.5;
                                             4F2BAB3269592E53 CRC64;
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    DB 1;
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    Length 167;
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PR04_LYCES
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PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS0101010; SCP_AG5_PR1_SC7_2; 1.
PROSITE; PS0101010; SCP_AG5_PR1_SC7_2; 1.
Plant defense; Pathogenesis related protein; Signal; Multigene family.
SIGNAL 1 24 BY SIMILARITY.
CHAIN 25 159 PATHOGENESIS RELATED LEAF PROTEIN 4.
POLICIENT 25 PATHOGENESIS PATHOGENESIS ACCID
MOD_RES 25 25 PATROLIDONE CARBOYFLIC ACID
DISULFID 68 136 BY SIMILARITY.
                                                                                                                                                                Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
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Matches 57; Conserv
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Q04108;
Q1-JUN-1994 (Rel. 29, Created)
O1-JUN-1994 (Rel. 29, Last sequence update)
O1-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis-related leaf protein 4 precursor (P4).
Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           van Kan J.A.L., Joosten M.H.A.J., Wagemakers C.A.M., van den Berg-Velthuis G.C.M., de Wit P.J.G.M., "Differential accumulation of mRNAs encoding extracellular and intracellular PR proteins in tomato induced by virulent and avirulent races of Cladosporium fulvum.", Plant Mol. Biol. 20:513:527(1992).
EMBL; M69247; AAA03615.1; -.
EMBL; A2634; CCAA01613.1; -.
HSSP: P04284; ICFE
HSSP: P04284; ICFE
InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                           use by non-profit institutions as lon modified and this statement is not remove entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Moneymaker; TISSUE=Leaf; MEDLINE=93043041; PubMed=1421154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                     INDUCTION: UPON INFECTION BY VIRILENT AND AVIRILENT RACES OF PATHOGENS, FOR EXAMPLE FUNGAL PATHOGEN C.FULVUM.
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION FOUND DURING AND DAYS 8 TO 12 AFTER INOCULATION WITH AN AVIRULENT VIRULENT PATHOGEN RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAINST PATHOGENS
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5; Mismatches
                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
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ches 61;
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DISULFID
SEQUENCE
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20-MAR-1987 (Rel. 04, Created)
01-JUN-1994 (Rel. 29, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Pathogenesis-related leaf protein 6 pr
protein P1) (P14) (P14A) (PR protein).
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Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                          "Two PR-1 genes from tomato are differentially regulated and reveal a novel mode of expression for a pathogenes; related gene during the hypersensitive response and development."
Mol. Plant Microbe Interact. 10:624-634(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           van Kan J.A.L., Joosten M.H.A.J., Wagemakers C.A.M., van den Berg Velthuis G.C.M., de Wit P.J.G.M.; of "Differential accumulation of mRNAs encoding extracellular and intracellular PR proteins in tomato induced by virulent and avaces of Cladosporium fulvum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Moneymaker; TISSUE=Leaf; MEDLINE=93043041; PubMed=1421154;
                                                     unfamiliar
                                                                       "Amino acid sequence of the
from viroid-infected tomato
                                                                                                                                               Lucas J., Camacho Henriquez
                                                                                                                                                                                               SEQUENCE OF 25-159.
                                                                                                                                                                                                                                                                                                                                            MEDLINE=97348583; PubMed=9204567;
Tornero P., Gadea J., Conejero V.,
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tornero P., Rodrigo T., Conejero V., Vera P.;
"Nucleotide sequence of a cDNA encoding a pathogenesis-related protein, pl.pl4, from tomato (Lycopersicon esculentum).";
Plant Physiol. 102:325-325(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. MILL; T
MEDLINE=94151430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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61; Conser
                       iar proteins.";
4:2745-2749(1985)
                                                                                                                                                                                                                                                                                                                                                                                               VFN8; TISSUE=Leaf;
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                                                                                                                                                                       Rutgers;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20:513-527(1992).
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145
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                                                                  'pathogenesis-related' leaf protein reveals a new type of structurally
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Pred. No. 1.2e-15;
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                                                                                                                                                                                                                                                                                                                                                 Vera P.;
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                                                                                                                                             Henschen
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Best Local
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PR1_MEDTR
Q40374;
01-NOV-1997
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                CHAIN
MOD_RES
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
Plant defense; Pathogenesis~related pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A03379; VCTO14.
PIR; S26239; S26239.
PIR; S29628; S29628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION FOUND DURING AND DAYS 8 TO 12 AFTER INOCULATION WITH AN AVIRULENT VIRULENT PATHOGEN RESPECTIVELY.

-!- INDUCTION: UPON INECTION BY VIRULENT AND AVIRULENT PATHOGENS, FOR EXAMPLE FUNGAL PATHOGEN C.FULVUM. ALS
                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1;
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; 1CFE; 12-NOV-97.
InterPro; IPR001283; Allrgn_V5/Tpx1
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "NMR solution structure of the pathogenesis-related protein P14a.";
J. Mol. Biol. 266:576-593(1997).
i- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
AGAINST PATHOGENS. HAS ANTIFUNGAL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fernandez C., Szyperski T., Bruyere T.,
Wuethrich K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR.
MEDLINE=97220236; pubMed=9067611;
                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                 Fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                          143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INSECTS AG3/AG5;
                                                                                                                                                                                                                                EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGAN--QGWA 126
                                                                                                         ISCNYDPVGNWIGQRPY 159
                                                                                                                                   TLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                  DYLAVHNDARAQVGVGPMSWDANLASRAQNYA--NSRAGDCNLIHSGA--
                                                                                                                                                                                      SYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGATL 186
                                                                                                                                                            DFTGRAA--VQLWVSERPSYNYATNQCVGGKKCRHYTQVVWRNSVRLGCGRARCNNGWWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M69248; AAA03616.1; -. X68738; CAA48672.1; -. Y08804; CAA70042.1; -.
                                                                                                                                                                                                                                                                    l Similarity
61; Conser
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25 159

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68 136

109 115

131 145
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123
159 AA;
(Rel. 35, Created)
(Rel. 35, Last sec
                                                                                                                                                                                                                                                                    Conservative
                                        STANDARD;
                                                                                                                                                                                                                                                                                                                     127 N
17520 MW;
                                                                                                                                                                                                                                                                                 25.6%;
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SC7/SC14 AND PLANTS I
                                                                                                                                                                                                                                                                    Score 277.5;
Pred. No. 2.6e
13; Mismatches
                                                                                                                                                                                                                                                                                                                        MISSING (IN REF. 4).
; EA35A6C3AC0EF3F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          PATHOGENESIS - RELATED LEAF PROTEIN PYRROLIDONE CARBOXYLIC ACID.
                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; Signal; Multigene family;
                                        173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ramage P.,
                                                                                                                                                                                                                                                                    .6e-15;
es 54;
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AVIRULENT AND A
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                                                                                                                                                                                                                                                                                             Length 159;
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Best Local
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PRB1_TOBAC STANDARD; PRT; 177 AA.

P11670;

01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Basic form of pathogenesis-related protein 1 precursor (PRP 1).
Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID DISULFID DISULFID
                                                                                                                                         TOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001283; Allrgn_V5/Tpx1.
pfam; pF00188; SCP; 1.
pRINTS; pR00837; V5TPXLIKE.
proDom; pp000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01009; SCP_AG5_PRI_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PRI_SC7_2; 1.
Plant defense; Pathogenesis-related protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula (Barrel medic).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X79778; CAA56174.1; -. HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Szybiak-Strozycka U., Lescure N., Cullimore J.V., Gamas P., "A cDNA encoding a PR-1-like protein in the model legume Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95175606; PubMed=7870819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41,
Pathogenesis-related
                                                                                                                                                                                                       151
                                                                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                                      123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rt Physiol. 107:273-274(1995).
FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAINST PATHOGENS
                                                                                                                                                                                                       DDKGTFMTCNYDPPGNYYGERPY
                                                                                                                                                                                                                                    TG-ATLTLCLYNPHGNVQGQSPY
                                                                                                                                                                                                                                                                      IFWGSGVGWNPAQAVSAWVDEKQFYNYWHNSCVDGEMCGHYTQVVWGSTTKVGCASVVCS
                                                                                                                                                                                                                                                                                                  QGWAS-YRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCA 181
                                                                                                                                                                                                                                                                                                                                    SRSFKNQFLIPQNIARAAVGLRPLVWDDKLTHYAQ-WYANQRR-NDCAL-EHSNGPYGEN 90
                                                                                                                                                                                                                                                                                                                                                                    SNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGAN 122
                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
60; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19760 MW;
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42.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 268.5;
Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

PATHOGENESIS-RELATED PROTEIN PR-1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      898B00C9CD72DE4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      .4e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
                                                                                                                                                                                                                                                                                                                                                                                                        59;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 57
                    PRIA_LYCES STANDARD; PRT; 175 AA.

Q08697;
Q10-CQT-1996 (Rel. 34, Created)
Q1-CCT-1996 (Rel. 34, Last sequence update)
Q1-CCT-1996 (Rel. 34, Last sequence update)
Q1-CCT-1996 (Rel. 34, Last annotation update)
Q1-CCT-1996 (Rel. 34, Last annotation update)
Q2-CCT-1996 (Rel. 34, Last annotation update)
Q3-CCT-1996 (Rel. 34, Last annotation update)
Q4-CCT-1996 (Rel. 34, Created)
Q4-CCT-1996 (Rel. 34, Cre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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prINTS; PR00837; V5TPXLIKE.
proDom; PD000542; Allrgn_V5/Tpx1; 1.
sMARF; SM00198; SCP; 1.
pROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
pROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carnes M., Ryals J.;
"Isolation and sequence of a genomic clone encepathogenesis related protein 1 from Nicotiana Plant Mol. Biol. 12:595-596(1989).
-i- FUNCTION: PROBABLY INVOLVED IN THE DEFENSI AGAINST PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant defense; Pathogenesis-related protein; Multigene family; SIGNAL 1 23 BY SIMILARITY.

CHAIN 24 177 BASIC FORM OF PATHOGENESIS-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X14065; CAA32228.1;
PIR; S04728; S04728.
HSSP; P04284; ICFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-cv. Xanthi;
Payne G., Middlesteadt W., Desai N., Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; eudicotyledons; core Asteridae; euasterids I; Solanales; Solanaceae; Nic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGSNATADEYLAPHNQARAAYGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
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SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANQGWASYKARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNGWFFITCNYDPPGNFIGQRPF 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGATLTLCLYNPHGNVQGQSPY
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PROSITE: PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE: PS01010; SCP_AG5_PR1_SC7_2; 1.

PROSITE: PS01010; SCP_AG5_PR1_SC7_2; 1.

PATHOGENES: Pathogenesis - related protein; Signal; Multigene family.

SIGNAL 1 21 POTEMTIAL.

CHAIN 22 175 PATHOGENESIS-RELATED PROTEIN 1A1.

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1 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
2 01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
2 01-MI-2002 (TrEMBLrel. 21, Last annotation update)
3 01-MI-2002 (TrEMBLrel. 21, Last annotation update)
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9 11-M SEQUENCE FROM N.A.

Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Palm C.J., Bowser L., Jones T., Banh J., Kamiya A., Kawai J.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P. K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Boker J., Theologis A., Davis R.W.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. MEDLINE-98403884; PubMed-9734815;
MEDLINE-98403884; PubMed-9734815;
MAKAMURA Y., Sato S., Asamizu E., Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajin Tabata S.; Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned P1 and TAC clones."; physically assigned P1 and TAC clones."; Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M. Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Ka Q9FJY1 SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI_TaxID=3702; Q9FJY1; PRELIMINARY; PRT; 185 A Kaneko T., Miyajima eudicots; Rosidae; protein) Tracheophyta; Kawai J.,

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Wiltse C.C., Frederiksen R.A., Bhandhufalck A., Hu.
"Induced resistance responses in maize.";
MOI. Plant Microbe Interact. 11:643-658(1998).
EMBL; U82200; AAC25629.1; -.
EMBL; U82200; AAC25629.1; -.
HSSP; P04284; ICFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
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PROSITE; PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.

SEQUENCE 163 AA; 17224 MW; 8331850F13365219
                                                                                                                                                                                                                                                                                                                                                                           Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1
PRINTS; PR00837; V5TPXLIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY093248; AAN
HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=98313983; PubMed=9650297;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pathogenesis related protein-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
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                            ACLLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KESTVLTICFYNPPGNVIGQKPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GWAS--YRARPAEVVALWVAEGRYYTHANNTCAAGROCGTYTQVVWRNTAEVGCAQASCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAAAKAFTDAHNKARAMVGVPPLVWSQTLEAAASRLARYQRNQKKCEFASLNPGKYGANQ
ACLLALAMAAIVVAPC ---
                                                          Similarity 39. 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.1%;
                                                                        30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                          Score 331; DB
Pred. No. 1.2e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 348.5; DB 10;
Pred. No. 6.7e-19;
7; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163
                                                        DB 10;
|.2e-17;
|es 61;
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-TAQNSPQD-YVDPHNAARA
                                                                                                                                                                                                                                                                                                   M., Thomas S.
Hulbert S., U
                                                                                                                    CRC64;
                                                                                      Length 163;
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RESULT
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Best Local S
Matches 75
                                                                                                                                                                                                                                                                          Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                           TISSUE-PISTLI,
Tomimoto Y., Ikehashi H., Kakeda K.,
"A pistil-specific PR-1 like protein
sequence and genealogical position.",
Breeding Sci. 49:97-104(1999).
EMBL, AB015047; BAA34937.1; -.
HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Theaceae; Camellia.
                                                                                                                                                                                                                                                                                                          InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
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01-MAY-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                ProDom; PD00054; SMART; SM00198;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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"Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomimoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-PISTIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Camellia sinensis (Tea).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR-1 like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4442;
                                 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGA-TLTLCLYNPHGN 196
                                                      YNPH-GNVQGQSPY 203
                                                                                                  AEVVALWVAEG-RYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCA-TGATLTLCL
                                                                                                                          NSARAEVGVDPLKWSYSLANAASRLVRYQKNYMHCEFADMTGQLQYGSNQMWSDYSAKPP
                                                                                                                                       NQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADV-GASPYGANQGWASYRAR-P
                                                                                                                                                                       ILPVLLLVIC -- HSSTHLLADHPIAARWVPPG--
                                                                                                                                                                                             LLLATLLALCAAPAPTH-----GARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVGVGPVSWDDTVAAYAQSYAAQ--RQGDCKLIHSG-GPYGENLFWGSAGADWSASDAVG
                                YYPHPGNLGGQRPY
                                                                             REVVEYWVNSGKKHYRYTHNYCVRNQNCGPYKQVVWEKTEMVGCAQGVCGNNNGSLSICF
                                                                                                                                                                                                                   Similarity 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sci.
                                                                                                                                                                                                                                                                191 AA;
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamaguchi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                of PR-1-like proteins 46:293-293(1996).
                                                                                                                                                                                                                                                                                                2; Allrgn_V5/Tpx1; SCP; 1.
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                                  191
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21591 MW;
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38.7%;
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10,
21,
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                                                                                                                                                                                                                             Score 325.5; DB 1
Pred. No. 3.7e-17;
                                                                                                                                                                                                                                                              POTENTIAL. 6764CEA8CBF80467 CRC64;
                                                                                                                                                                                                                   Mismatches
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of Camellia,
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                                                                                                                                                                                                                                         DB 10; Length
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                                                                                                                                                                      -----AARQFVDAH
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                                                                                                                                                                                                                   Gaps
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Best Local
                                                                                       08W084, PRELIMINARY; PRT; 167 AA.
Q8W084; PARELIMINARY; PRT; 167 AA.
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
          Oryza sativa (Rice).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; iPR001283; Allrgn_V5/Tpx1.
Pfam; pF00188; SCP; 1.
PR.NTS; PR00837; V5PPXLIKE.
PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
SMART; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
SEQUENCE 164 AA; 18397 MW; 840F99DB9FA7DF39 CRC64;
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                                                                      Putative pathogenesis-related OSJNBA0091E23.7.
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HSSP; P04284; ICFE.
InterPro: TDBOOCCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
Submitted (JUN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TremBLrel.
01-NOV-1999 (TremBLrel.
01-JUN-2002 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1999) to
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01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                        149
                                                                                                                                                                                                                                                                            128
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                                                                                                                                                                                                                                                     89
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                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                GALSGAEAVKLWVNEKSDYIYASNTCSDGKQCGHYTQVVWRTSEWVGCAKVKCDNGGTFV
                                                                                                                                                                                                                                                              YRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGATLT 187
                                                                                                                                                                                                                                                                                               DYLDEHNRARTQVGVPPMKWHAG-AEQYAWNYAQQRK-GDCSLTHSNSNGLYGENLAWSG
                                                                                                                                                                                                                                                                                                                   EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASP-YGANQGWAS 127
                                                                                                                                                                                                       TCNYYPPGNYRGRWPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence of A. thaliana T1N24
                                                                                                                                                                                                                                                                                                                                                  63;
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ed (MAY-1999) to
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                                                                                                                                                                                                                                                                                                                                             28.9%; Sco
46.3%; Pro
ative 18;
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12,
21,
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Last sequence update)
Last annotation updat
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Pred. No. 2.5
                                                                                protein.
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RESULT 6
Q43489
ID Q4348
AC Q434
AC Q434
DT 01-N
DT 01-N
DT 01-N
DT 01-N
DT 01-I
OC EUK
CC EUK
CC EUK
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OX NCB
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RR RA EK
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Best Local S
Matches 73
                                                                         Signal
SIGNAL
                                                                                                                                                                                                                                                                                                                                          Bryngelsson T., Sommer-Knudsen J., Greyerson. .....

Bk B., Thordal-Christensen H.;

Purification, characterization and molecular cloning of basic PR-1-

"Purification, characterization and molecular cloning of basic PR-1-
                                                                                                                                                                                      EMBL; X74939; CAA52893.1; ...
HSSP; P04284; 1CPE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PRODOm; PD000542; Allrgn_V5/Tpx1; 1.
       SEQUENCE
                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. PALLAS; TISSUE=LEAF; MEDLINE=94281675; PubMed=8012045; BryngeLsson T., Sommer-Knudsen J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Str.
Spermatophyta; Magnollophyta;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      043489;
01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-JUN-2002 (TIEMBLIEL 21, Last annotation updat
PR-la pathogenesis related protein (HV-la) precur
                                                                                                                                                                                                                                                                                                                                type pathogenesis related proteins from barley Mol. Plant Microbe Interact. 7:267-275(1994).
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Interpro; IpR001183; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PFINITS; PR00837; V5TPXLIKE.
PRINTS; PR000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                        PROSITE;
                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4513;
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Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki tiva nipponbare(GA3) genomic
clone:OSJNBa0091E23.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVALWVAE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASKLAICS-----LEVL-----AVVAATMEHCSDAQNSPQD-YLSPQNAARSAVGVG
                                                                                                                                            SM00198; SC
E; PS01009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167
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                                                                                                                        PS01010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS01009; SCP_AG5_PR1_SC7_1;
PS01010; SCP_AG5_PR1_SC7_2;
167 AA; 18334 MW; 40AE3I
    164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                   25
25
    AA;
                                                                                                                                                                  SCP;
                                                                                                                                                                Allrgn_V5/Tpx1; 1.
CP; 1.
                                                                                                                 SCP_AG5_PR1_SC7_1;
SCP_AG5_PR1_SC7_2;
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164
  17440
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yta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                           (HV-lA)
                                            PR-1A PATHOGENESIS RELATED PROTEIN
                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 309; DB 10;
Pred. No. 5.5e-16;
1; Mismatches 68;
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_SC7_2; UNKNOWN_1.
_40AE3EA728443D2E CRC64;
063F219DEFE7E548 CRC64;
                                                                                                                   164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Embryophyta; Tracheophyta;
a; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pooideae;
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Best Local Similarity
                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                               InterPro; IPRO01283; Allrgn_V5/Tpx1.

pfam; PF00188; SCP; 1.

PRINTS; PR00837; V55TXLIKE.

ProDom; PD000542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

SMART; SM00198; SCP, AG5_PR1_SC7_1; 1.

PROSITE; PS010109; SCP_AG5_PR1_SC7_2; 1.

PROSITE; PS011010; SCP_AG5_PR1_SC7_2; 1.

SEQUENCE 172 AA; 18830 MW; 6E94C8CADAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thallana (Mouse-ear crees).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core ex

Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pathogenesis related protein - like (Pathogenesis related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obermaier B., Deutschenbaur Mayer K.F.X.; Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Obermaier B., Deutschenbaur S., Piravandi E., Hoheisel J., Heijnen L., Vos P., Mewes H.W., Mayer K.F.X., Schueller C., Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               081889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/G
EMBL; AL031394; CAA20586.1; -.
EMBL; AL151584; CAB80090.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                      123
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                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASC-ATGATLTLCLYNPHGNVQGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAILLALAMAAAMVN------LSQAQN-----SPQDYLSPHNAARAAVGV
                    QGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT 182
                                                                    SNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGAN 122
                                                                                                                                                                                               Similarity
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                                                                                                                                                                                               28.3%;
44.7%;
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                                                                                                                                                                                               Score 307.5;
Pred. No. 7.
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                                                                                                                                                                        Mismatches
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                                                                                                                                                                     7.3e-16;
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                                                                                                                                                                                                                      DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a; Tracheophyta;
eudicots; Rosidae;
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RESULT 9
Q39188
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Best Local S
Matches 63
                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry.
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabic
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00837; V5TPXLIKE.

ProDom; PD000542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

SEQUENCE 184 AA; 20384 MW; OFFB1BEBF4A1D565 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequences of two PR-1 pseudogenes cv. Wisconsin 38.";
Nucleic Acids Res. 18:3404-3404(1990).
EMBL; X52555; CAA36790.1; -.
EMBL; P04284; ICEE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tobacco W38/1 PR-1 pathogenesis related protein.
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SEQUENCE FI
STRAIN=CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90287728; PubMed=2356132; Pfitzner A.J.P., Pfitzner U.M., G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=WISCONSIN 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NQGWASYR-ARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSGGYVVSCNYDPPGNFVGQSPY
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FROM N
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44.1%;
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Last annotation
in 1 precursor.
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Pred. No. 1
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1.4e-15;
hes 59;
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                                                                                                                       Embryophyta; Tracheophyta; edons; core eudicots; Rosid
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Q04106;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
Prb-1b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-CV. SAMSIN;
MEDIINE-92329719; PubMed-1627772;
MEDIINE-92329719; PubMed-1627772;
Eyal Y., Sagee O., Eluhr R.;
"Dark-induced accumulation of a basic pathogenesis-related (PR-1)
"Dark-induced accumulation of a basic pathogenesis related (PR-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                 transcript and a light requirement i
Plant Mol. Biol. 19:589-599(1992).
EMBL; X66942; CAA47374.1; -.
HSSP; P04284; ICFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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Submitted (MAR-1996) to the
EMBL; X96600; CAA65420.1; -.
HSSP; P04284; ICFE.
                                                                                                                                                                                                                                                                           PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1;
SMART; SM00198; SCP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRB-1B.
Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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ProDom; PD000542; Allrgn_V5/Tpx1;
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                                                                                                                                                                                                  PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
SEQUENCE 179 AA; 20120 MW; 7003FF0E1755152B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLYNPHGNVQGQSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFLAVHNRARAEVGVGPLRWDEKVAAYARNYANQ--RKGDCAMKH-SSGPYGENLAWSSG
  SQAQNSPQDYLNPHNAARRQVGVGPMTWDNRLAAFAQNYANQ~-RAGDCRMQHSG-GPYG
                                                SGSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNYDPPGNWVGEWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLTGRRAVDMWVDEQFDYDYDSNTCAWDKQCGHYTQVVWRNSERLGCAKVRCNNGQTFIT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                            Similarity
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26
169 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCP_AG5_PR1_SC7_1;
SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19330 MW;
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45.5%;
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                                                                                                 Score 302.5;
Pred. No. 1.8e
17; Mismatches
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hes 61;
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nes 52;
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Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
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Heijnen L., V.
Submitted (AU)
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Mayer K.F
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SEQUENCE FROM N.A.
Brooks S.,
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                                                                                                                                                                                                                                      Theologis A.;
"Full Length cDNA
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"Full length cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakano H., Liu S.X., Pham P.K., Yamada K., Banh J., Etgu P., Lee J. Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis "Full Length cDNA of gene T1611_210/AT4433720 (GI:77270321)."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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B., Deutschenbaur
, Vos P., Mewes H.
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01-NOV-1998 (TrEMBLrel. 08, L
01-UUN-2002 (TrEMBLrel. 21, L
Pathogenisis-related protein 1
PR-1.1.
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01-NOV-1998
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SMART; SM00198; SCP; 1.

PROSITE: PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE: PS01010; SCP_AG5_PR1_SC7_2; 1.

SEQUENCE 163 AA; 18492 MW; F0C568A56765C76E CRC64;
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                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1;
SMART; SM00198; SCP; 1.
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                                                                                                                                                                                                                                                                     PROSITE; PS01009; SCP_AG5_PR1_SC7_1; PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
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                                                                                                                                              SEQUENCE
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                                                                                                                                                  164
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                       Conservative
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164
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45.28;
                                                   27.3%;
39.7%;
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                                                                                                                                                  M.
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                       19;
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Pred. No. 3.9e
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                    Score 296.5; DB 10
Pred. No. 4.6e-15;
9; Mismatches 63;
                                                                                                                                                                                PATHOGENISIS-RELATED PROTEIN
                                                                                                                                                  6D652EB2646B8A44 CRC64;
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annotation
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                                                                                 DB 10;
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54;
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                                                                                 Length
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                                                                                        164;
                       29;
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RESULT
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          Theologis A.;

"Full Length cDNA of gene At4g33710 (G
Submitted (DEC-2001) to the EMBL/GenBa
EMBL; x96600; CAA65419.1; -.
EMBL; AL031394; CAA20584.1; -.
EMBL; AL161884; CAB80088.1; -.
EMBL; AV070411; AAL49907.1; -.
HSSP: P04284; ICFE.
InterPro; IPR00183; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
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Q39187;
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Pathogenesis-related protein 1 precursor (Pathogenesis-related protein 1, precursor, 18.9K) (Putative pathogenesis-related protein 1,
                                                                                                                                                Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith Liee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Che Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Nauyen M., Palm C.J., Sakurai T., Satou M., Seki M. Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ypri ór pri or T16L1.200 or AT4G33710.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                              Obermaier B., Deutschenbaur
Heijnen L., Vos P., Mewes H.
Submitted (AUG-1998) to the
                                                                                                                                                                                                                                  Yamada K., Banh J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. C24;
Kloska S., Schuster
                                                                                                                                                                                                                                                                                                                              Submitted
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                                                                                                                                                                                                                                                                                                                                                       Obermaier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT--GATLTLCLYNPHGNVQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVALWVA
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  PR00837;
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  V5TPXLIKE
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                                                                                                           EMBL/GenBank/DDBJ
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                                                                                                                        (GI:15235052).";
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dons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
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, Schueller C.,
J databases.
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                                                                                                                                                                                                       Goldsmith A.D.,
M., Wu H.C.,
hen H., Cheuk R.,
                                                                                                                                                                   Seki M.,
                                                                                                                                                                                                                                                                                                                                                            Lemcke
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, Bevan
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RESULT 14
Q94F73
ID Q94F7
AC Q94F7
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-DE
CO Triti
OC Eukar
OC Sperm
OC Triti
OC NCBL
RN (L)
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Best Local S
Matches 71
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Best Local
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pathogenesis-related protein 1.
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
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SMART; SM00198; SCP; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF384143; AAK60565.1; ...
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; UNKNOWN_1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
SEQUENCE 164 AA; 17537 MW; 5E2605216D1F9E25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
YU L., Niu J.-S., Ma Z.-Q., Chen P.-D., Liu D.-J.;
"Cloning and characterization of pathogenesis-related protein wheat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q94F73
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EKKDYDYGSNTCAAGKVCGHYTQVVWRASTSIGCARVVCNNNLGVFIT-CNYEPRGNIIG
                            EGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT--GATLTLCLYNPHGNVQG 199
                                                                                                      GAVTWSTKLQGFAQSYANQ-~RINDCKLQHSG-GPYGENIFWGSAGADWKAADAVNAWVG 101
                                                                                                                                                APLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVALWVA 141
                                                                                                                                                                                                               LAILLALAMSAAMAN.
                                                                                                                                                                                                                                                               LATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NHARDDVSVPHIKWHAG-AARYAWNYAQRRKRDCRLIHSNSRGRYGENLAWSSGDMSGAA
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70; Conserv
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166 AA;
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166 POTENTIAL.
18952 MW; A32EEF66245CDC5B CRC64;
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7.2e-15;
hes 72;
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les 63;
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Matches 60
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                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. SHIN SUYO TSUKEMIDORI;
COOls H.J., Ishii H.;
"Pre-treatment with Acibenzolar-S-methyl Systemically Primes
"Phenylalanine Ammonia Lyase (PAL1) Gene Expression in Cucumber
"Phenylalanine Ammonia Lyase (PAL1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cucumis sativus (Cucumber).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pathogenesis-related protein 1-la (Fragment).
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                                                                                                                                                                                            EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQ~--RRQGGCAFADVGASPYGANQGW 125
                                                            GTFIICNYEPRGNFLYQRPY
                                                                                                                                 ASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCA--TG 183
                                                                                                                                                                       DFYGYHNVARAQYGYGFIEWDKTVAS-----FAQQYANRRLNDCRLVNSG-GPYGENIAW 60
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                                                                                      ATLTLCLYNPHGNVQGQSPY
                                                                                                                  GSPDLSAKDAVQLWVDEKPFYNYETNTCAAGELCGHYTQVVWRKSVRIGCAKVRCTDNIG 120
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14; Mismatches 55
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Minimum DB
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Gapop 10.0 , Gapext 0.5
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             PR-1 like protein
Zea mays pathogene
Amino acid sequenc
Arabidopsis thalia
Arabidopsis thalia
Amino acid sequenc
                                                                                                                                                                                                                       Description
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Arabidopsis thalia
Arabidopsis thalia
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NTS	ALIGNMENTS					
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Zea mays pathogene Arabidopsis pathog	AAY44004	20	156 135	22.1	240 238	43
Herbicidally activ	130	23	161		243	41
CO .	83	13	150	2	244.5	40
Arabidopsis thaila A. thaliana enviro	AAY77966	21	176	٧.	246	ω α α
thali	AAG41288	212	161	, ω	257	37
is	AAG41289	21	148	ω	257	36
-rela	AAR28352	13	160	ω.	259.5	35
nesis.	AAR28354	3	159	w •	259.5	34
PR-1	AAW83433	20	177	4	260	ω u
Tobacco PR-1' prot		20	177	4	260	32
Tobacco PR-1 prote	AAP91384	10	177		260	Ψ
መ	AAR28350	13	159	. ·	277.5	30
Tomato pathogenesi	AAY43999	200	1 2 2	лυ	277.5	200
nathogena	AAK28331	2 L	7 12	'nО	278.5 5	7 0
Tomato pathogenesi	AAY44000	20	135	יי	281.5	26
Tobacco pathogenes	AAY44002	20	139	6.	284	25
\mathbf{L}	AAR07313	11	138	6.	284	24
encode	AAR05590	11	168	σ.	285	23
PR-la	AAW83432	20	168	σ.	286	22
PR-la pro		20	168		286	21
Tobacco PR-la prot		10	168	<u>ი</u>	286	20
an	AAP91057	10	168	<u>ه</u> ا	286	19
٠,		٥ د	160	: ת	280	2 7
Nicotiana tabacum	2001058	10	168	٦:	200	17
- 1	AAY44001	2 1	138	7 :	200	א ני
nlant	822	t	128	7	296	J ,
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acco parmoyene	- 4	2 6	1 / 1	٦.	300	7 5
ant patho	RO7	21	138	٦,	303	11

Malze; pathogen-related; PRI-CIU; plant; trantized mays. US2001049834-A1. 06-DEC-2001. 10-APR-2001; 2001US-0832320. 10-APR-2000; 2000US-195801P. (CRAN/) CRANE E H. (CRAN/) CRANE V C. CTane EH, Crane VC; WPI; 2002-121407/16. N-PSDB; ABA96417, ABA96418.	ID AAM48742 st XXX AAM48742; AC AAM48742; XX DT 02-APR-2002 XX Maize PR1-C	RESULT 1
Malze; patnogen-related; PRI-CIU; plant; transgenic. Zea mays. US2001049834-A1. 06-DEC-2001. 10-APR-2001; 2001US-0832320. 110-APR-2000; 2000US-195801P. (CRAN/) CRANE E H. (CRAN/) CRANE V C. CYANE EH, CYANE VC; WPI; 2002-121407/16. WPF; 2002-121407/16.	742 standard; Protein; 203 AA. 742; R-2002 (first entry) PR1-C10 SEQ ID NO 2	

New nucleic acid encoding a pathogen related protein isolated maize and designated PRI-C10, useful for transforming plants i enhanced disease resistance

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SXCCCXXX
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05-MAR-1999

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29-MAR-1999

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06-APR-1999

11-APR-1999

21-APR-1999

23-APR-1999

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26-AMY-1999

06-MAY-1999

06-MAY-1999

06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid encoding pathogen-related protein PRI-C10. The nucleic acid is used plants for enhanced disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG47492 standard;
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                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                          termination sequence.
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Similarity 100.0%;
03; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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 9905-0121825
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Best Local Similarity 48.3
Matches 69; Conservative
25-FEB-1999

05-MAR-1999

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23-MAR-1999

25-MAR-1999

29-MAR-1999

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01-APR-1999

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16-APR-1999

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17; Mismatches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAR; tobacco; protein-synthesis independent gene; cyclohexamide; systemic acquired reistance response; anti-pathogen; plant protection; maize; PR-1.
This sequence represents the maize PR-1 like protein, PR-1mz. The cDN encoding this sequence was isolated by screening a BTH-induced cDNA library of maize. The library was screened using a probe matching to the PR-1 barley clone HVPR1BR. The cDNA encoding this sequence,
                                                                                                                                                                    New DNA contg. plant systemic acquired resistance genes - and transgenic plants contg. them, impart disease and pest resistance, also Arabidopsis gene promoter to control DNA transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-1999;
22-OCT-1999;
                                                                                                                     Claim 21; Page 70-71; 85pp; English.
                                                                                                                                                                                                                                                                                                                                            Alexander DC,
                                                                                                                                                                                                                                                                                                                                                                                      (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JAN-1994;
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DB; AAQ99804.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GWAS--YRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCA 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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99US-0160980.
99US-0160981.
                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0181271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0161404
99US-0161405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-IB00002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0161359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0161406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0160989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.0%;
47.6%;
                                                                                                                                                                                                                                                                                                                                            Uknes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 347.5;
Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
                                                                                                                                                                                                                                                                                                                                            SJ,
                                                                                                                                                                                                                                                                                                                                            Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .9e-24
                                                                                                                                                                                                                                                                                                                                            ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY29944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ99800-Q99803 and AAQ99805 are all used in recombinant/chimaeric DNA molecules of the invention. The DNA sequences were isolated by differential screening of a cDNA library, followed by analysis by Northern hybridisation to RNA in the presence and absence of cyclohexamide. The genes are used in the creation of transgenic plants All of these sequences confer anti-pathogenic properties to transgenic plants. Transgenic expression of 2 or more of the recombinant molecule of the invention that encode anti-pathogenic proteins provides a synergistic increase in plant protection, and may also offer protection against a wider range of pathogens.
                                                                                                                                                                        26-FEB-1998;
27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                   regulation; expression; disease resistance; genetic manipulation; tobacco mosaic virus; cucumber mosaic virus; ringspot virus; necrosis virus; maize dwarf virus; viroid; bacterial; insect;
                                                                                                                                                                                                                                                                                                                                                                            Zea mays; maize; pathogenesis-related class I;
                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays pathogenesis-related class I PR-1#83 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                   New promoter sequences
                                                                                                                     Crane VC
                                                                                                                                                                                                                 11-FEB-1999;
                                                                                                                                                                                                                                           02-SEP-1999.
                                                                                                                                                                                                                                                                      WO9943819-A1
                                                                                                                                                                                                                                                                                              Zea mays
                                                                                                                                                                                                                                                                                                                          nematode; fungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY29944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY29944 standard; Protein;
                                                                                                                                              (PION-) PIONEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197
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                                                                             1999-527621/44
DB; AAZ21207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LWVAEGRYYTHANNTCAAGROCGTYTOVVWRNTAEVGCAQASCATGA-TLTLCLYNPHGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVGESPY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWVSEKQYYDHDTNSCAEGQVCGHYTQVVWRDSTAIGCARVVCDNNAGVFIICSYNPPGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVGVGPVSWDDTVAAYAQSYAAQ--RQGDCKLIHSG-GPYGENLFWGSAGADWSASDAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
73; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                        98US-0076100
98US-0079648
                                                                                                                                                                                                                 99WO-US03011
                                                                                                                                               HI-BRED INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.5%;
                                                   from pathogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score 331; DB 16;
Pred. No. 5.6e-23;
1; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                           PR-1; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 163;
                                                   genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                    of
                                                    maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32:
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a
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AAZ21186 to

AA221190

represents the nucleotide

sequences

for

promoters

Example 3; Page 73-74; 86pp; English

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolated from a family of maize (Zea mays) genes encoding pathogenesis related (PR-1) proteins. The promoters are useful for expressing heterologous genes (including genes for disease resistance) in plants, especially dicots, or monocots i.e. maize. The promoters are useful for the genetic manipulation of plants to exhibit specific phenotypes, particularly enhanced resistance to pathogen-caused disease. Pathogens include viruses such as tobacco or cucumber mosaic virus, ringspot virus, necrosis virus, and maize dwarf virus, and viroids, bacteria, insects, nematodes and fungi. The present sequence represents a maize PR-1 protein given in the present invention.
The present sequence represents a polypeptide which has antibacterial activity. The antibacterial protein and its polynucleotide can be use for the creation of a plant with resistance against pathogenic microbacterial protein and the protein and the protein and the protein activity.
                                                                                                                                                     (MITU ) MITSUBISHI CHEM CORP.
(BADA-) BADAN PENGKAJIAN DAN PENERAPAN TEKNOLOGI.
(PAKR-) PT PAKRIE BROS.
(BIOI-) BIOINDUSTRY KYOKAI SH.
(DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
                                                                                                                                                                                                                                                                            02-APR-2002
                                                                                                                                                                                                                                                                                                   JP2002095477-A.
                                                                                                                                                                                                                                                                                                                         Elaeis guineensis
                                                                                                                                                                                                                                                                                                                                                  Antibacterial protein;
                                                                                                                                                                                                                                                                                                                                                                                                                        ABB77767;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB77767 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                         Claim 1; Page 9-10; 13pp;
                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of an antibacterial protein.
                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2002 (first entry)
                                                                               New protein and its gene, useful resistance to pathogenic microbes
                                                                                                                                                                                                                             20-SEP-2000; 2000JP-0285905.
                                                                                                                                                                                                                                                     20-SEP-2000; 2000JP-0285905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 ACLLLATLIALCAAPAPTHGARVIMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGA-TLTLCLYNPHGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVA 137
                                                                                                                                2002-439987/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVGESPY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWVSEKQYYDHDTNSCAEGQVCGHYTQVVWRDSTAIGCARVVCDNNAGVFIICSYNPPGN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVGVGPVSWDDTVAAYAQSYAAQ--RQGDCQLIHSG-GPYGENLFWGSAGADWSASDAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACLLALAMAAIVVAPC-----TAQNSPQD-YVDPHNAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                     ABL59008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑĀ;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.5%;
                                                                                                                                                                                                                                                                                                                                                  microbe
                                                          Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 331; DB 20;
Pred. No. 5.6e-23;
1; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                  resistance; plant.
                                                                                    for
                                                                                             creating
                                                                                             plants with high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
            microbes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                       used
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           Qy
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В Qy

В Qy QΥ

В QΥ

Дb

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Query Match
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                         25-FEB-1999
05-MAR 1999
09-MAR 1999
23-MAR 1999
25-MAR 1999
25-MAR 1999
06-APR 1999
08-APR 1999
08-APR 1999
116-APR 1999
23-APR 1999
24-MAY 1999
06-MAY 1999
06-MAY 1999
07-MAY 1999
11-MAY 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hybridisation assay; genetic mapping; gene expression termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG47493 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVSAHNAARAAVGVGPVSWDNTVAAYAQNYANQ--RIGDCQLVHSG-GPYGENLFWGSG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICNYKPPGNIVGQRPY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       2000EP-0301439
990S-0132484
990S-0132485
990S-0132487
990S-0132487
990S-0134256
990S-0134218
990S-0134211
990S-0134211
990S-0134768
990S-0134768
990S-013494
990S-0135324
                                                                                                                                                                                   99US-0130510.
99US-0130891.
99US-0131449.
99US-0132048.
99US-0132407.
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99US-0130077.
99US-0130449.
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99US-0127462.
99US-0128234.
99US-0128714.
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45.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 322;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23;
.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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16.JUN-1999 18.JUN-1999 19.JUN-1999 20.JUN-1999 21.JUN-1999 22.JUN-1999 23.JUN-1999 24.JUN-1999 25.JUN-1999 26.JUN-1999 27.JUN-1999 28.JUN-1999 28.JUN-1990 28.JUN-1990 28.JUN-1990 28.JUN	24 - MAY - 1999; 25 - MAY - 1999; 27 - MAY - 1999; 28 - MAY - 1999; 01 - JUN - 1999; 03 - JUN - 1999; 04 - JUN - 1999; 07 - JUN - 1999; 10 - JUN - 1999; 10 - JUN - 1999;
990S-0139159 990S-0139452 990S-0139453 990S-0139454 990S-0139456 990S-0139461 990S-0139461 990S-0139461 990S-0139463 990S-0139463 990S-0139463 990S-0139463 990S-0140354 990S-0140354 990S-0140354 990S-0140354 990S-0140354 990S-0140354 990S-0140353 990S-0140353 990S-0140353 990S-0140353 990S-0140353 990S-0144335 990S-0145368	990S-0135629 990S-0136021 990S-0136392 990S-0136782 990S-0137222 990S-0137528 990S-0137502 990S-0137502 990S-0137502 990S-0138640 990S-0138640
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99US-0148319 99US-0148561 99US-01485684 99US-01493684 99US-01493684 99US-0149902 99US-0149902 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-0151069 99US-015069 99US-0160980 99US-0161406 99US-0161406 99US-01613569	99US-0146389 99US-0147038. 99US-0147204. 99US-0147192. 99US-0147192. 99US-0147260. 99US-0147303. 99US-0147416. 99US-0147416. 99US-0147935. 99US-0147935.

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RESULT 8
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28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                             25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO:
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l Similarity 49.2%;
62; Conservative 1
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99US-0161993.
99US-0162142.
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; Pred. No. 1.1e-21;
14; Mismatches 47;
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990S-0136732
990S-0137528
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990S-0137522
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990S-0139453
990S-0149463
990S-014953
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99US-0146388. 99US-0146389. 99US-0147038. 99US-0147204. 99US-0147302.

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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an antibacterial protein of Wasabia japonica. The protein can be used in an antibacterial agent and a functional food.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-439986/47.
N-PSDB; ABL59001.
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 13-14; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-SEP-2000; 2000JP-0284178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP2002095475-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibacterial protein; antibacterial agent; food; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of an antibacterial protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB77765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibacterial protein gene of Wasabia japonica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 IGQKPY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 QGQSPY 203
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                                                                                                                                                                                                                                                                          Local Similarity es 72; Conserv
                                                                           46
                                                                                                                       83
                                                                                                                                                                                                             23 LLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVG
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                                                                        VGVPPLVWSQTLEAAASRLARYQRNQKKCEFASLNPGKYGANQLWAKGLVAVTPSLAVET
                                                                                                                                                                            LLLILAALVGA-----IVLP-----SKAQD-----SPQDYLRVHNQARAAVG
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l Similarity 48.4%;
61; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                 161 AA;
                                                                                                                                                                                                                                                                                Conservative
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99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                          28.0%; Score 304; DB 23; 39.8%; Pred. No. 1.8e-20; Live 20; Mismatches 61;
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; Pred. No. 1.4e-21;
15; Mismatches 47; Indels
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                                                                                                                                                                                                                                                                                                                               Length 161;
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                                                                                                                                                                                                                                                                                                                                   Pathogenesis-related proteins used for expression in plants to invading pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pathogenesis-related protein; Nicotiana tabacum cv. Samsun NN; pNtSNNcPRlc/83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP91059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP91059 standard; protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1989-087235/12
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                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                               Fig 4; ; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Pfitzner UM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAR-1989
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            149
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                                  184
                                                                               125
                                                         89
                                                                                                      36
                                                                                                                             69
            GYIVSCNYDPPGNVIGKSPY 168
                                                                                                                  EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGANQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KANYNYPSNTC--NGVCGHYTQVVWRNSVRLGCAKVRCNNGGTIIVCNYDPPGNYVNQKP
                                  ATLTLCLYNPHGNVQGQSPY
                                                                    WASYR-ARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATG 183
                                                                                                       DYLDAHNTARADVGVEPLTWDNGVAAYAQNYASQ------LAADCNLVHSHGQYGENLA 88
                                                       WGSGDFLTAAKAVEMWVNEKQYYAHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNG
                                                                                                                                                    63;
                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tabacum cv. Samsun
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                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Signal peptide"
31..168
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                                                                                                                                                               28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                          ΑP,
                                  203
                                                                                                                                                    15;
                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                          Goodman
                                                                                                                                                                                                                                                                                                                                              and regulatory sequences - to enhance hypersensitive response
                                                                                                                                                    Mismatches
                                                                                                                                                               304;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                          M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (P-R) protein encoded by
                                                                                                                                                              DB
.9e
                                                                                                                                                 10;
-20;
50;
                                                                                                                                                                         Length 168;
                                                                                                                                                    Indels
                                                                                                                                                    12;
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160
                                                                                                                             124
                                                                                                                                                    ω
RESULT 12
AAY44003
ID AAY44
XX
AC AAY44
XX
AC AAY44
XX
XX
DT 21-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
AAR07314
                                                                                                                                                                                                                                                                                                      В
                                                                                                                                      QУ
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                                                                                                                                                                                   Ωy
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                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-OCT-1989;
24-MAR-1989;
20-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR07314 standard;
                                                                                                                                                                                                                                                                                                                          This is the sequence of the plant pathogenesis-related protein (PRP), PR-1b. It confers systemic acquired resistance to plants. The corresp. DNA is used, in a chimeric construct, to produce transgenic plant cells or -tissues with the ability to regenerate into plants which are disease resistant. See also AAQ06179-80, AAQ06182-86, AAQ06199-Q06208 and AAQ06829.
                                                                                                                                                                                                                                                                                                                                                                                                                              Disease-resistant transgenic plants - inducible pathogenesis-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic plants; disease resistance; chimeric plant pathogenesis-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR-1b plant pathogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-313983/42.
N-PSDB; AAQ06181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP392225-A.
            21-DEC-1999
                                    AAY44003;
                                                          AAY44003
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Example 15; page 22; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stinson JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ryals JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CIBA ) CIBA GEIGY AG
                                                                                                                   118
                                                                                                                                                                                     123
                                                                                                                                        183
                                                                                                                                                                59
                                                                                                                                                                                                                                   69
                                                                                                                                                                                                             6
                                                                                                                                 GATLTLCLYNPHGNVQGQSPY
                                                                                                                                                                                   QGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT 182
                                                                                                                                                                                                                                  EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN-- 122
                                                                                                                  GGYVVSCNYDPPGNVIGOSPY 138
                                                                                                                                                                                                             DYLDAHNTARADVGVEPLTWDNGVAAYAQNYVSQ
                                                                                                                                                                QGSGDFMT-AAKAVEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVKCNN 117
                                                                                                                                                                                                                                                        1 Similarity
65; Conserv
                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alexander DC,
R, Neuhaus J-M,
                                                                                                                                                                                                                                                                                                      138
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-0425504.
89US-0329018.
89US-0368672.
                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90EP-0105336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                        27.9%; Score 303; D; 46.1%; Pred. No. 1.8 tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodman RM,
Moyer MB;
                                                                                                                                        203
                                                         139
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                                                          AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                obtd. using encoding a from infected plants.
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                                                                                                                                                                                                                                                        DB 11;
1.8e-20;
hes 47;
                                                                                                                                                                                                             -- LAADCNLVHSHGQYGENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Payne
                                                                                                                                                                                                                                                                                Length 138;
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                                                                                                                                                                                                                                                           14;
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58

4.

밁 Qy В δÃ Вb γQ

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RESULT 13
AAY44005
ID AAY44
AC AAY44
AC AAY44
AC 21-DE
XX 21-DE
XX Predi
XX Predi
KW homol
KW site
XX Sea m
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prediction; secondary structure; alignment; evolutionary conservation;
homology; periodicity; co-variation analysis; antigenic site;
site directed mutagenesis; interaction.
   Zea mays
                      site directed
                                Prediction; secondary structure; alignment; evolutionary conservation, homology; periodicity; co-variation analysis; antigenic site;
                                                                Maize pathogenesis related
                                                                                       21-DEC-1999
                                                                                                          AAY44005;
                                                                                                                                AAY44005 standard; Protein; 141
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Column 371-374; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Predicting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Benner SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-570766/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tobacco
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                                                                                                                                                                                     119
                                                                                                                                                                                                          183
                                                                                                                                                                                                                                                   123
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                                                                                                                                                                                                                                                                                  GGYVVSCNYDPPGNVIGQSPY
                                                                                                                                                                                                          GATLTLCLYNPHGNVQGQSPY
                                                                                                                                                                                                                             QGSGDFMT-AAKAVEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVKCNN 118
                                                                                                                                                                                                                                                 QGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT 182
                                                                                                                                                                                                                                                                       DYLDAHNTARADVGVEPLTWDNGVAAYAQNYVSQ-----LAADCNLVHSHGQYGENLA 59
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathogenesis related
                                                                                                                                                                                                                                                                                                                                                             139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the folded structure of proteins
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                     (first entry)
                      mutagenesis;
                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-0857224
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                                                                                                                                                                                                                                                                                                                          27.9%;
46.1%;
                               co-variation analysis; antigenic
                                                               protein #3
                                                                                                                                                                                     139
                                                                                                                                                                                                        203
                      interaction.
                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                Score 303; DB 20;
Pred. No. 1.8e-20;
5; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                      Length 139;
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                                                                                                                                                                                                                                                                                                                 14;
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                                                                                                                                                                                                                                                                                                                                               Db
                                                                                                                                                                                                                                                                                                                                                                   Qγ
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                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                     Best
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
         25-FEB-2000; 2000EP-0301439
                               06-SEP-2000
                                                                                                                                                             18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                          61;
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     141 AA;
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sequences AAY43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as guides for site directed mutagenesis studies, and for
                                                               Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
Arabidopsis thaliana
                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 52828
                                                                                                                                                                                                                                                                                                                                                                                                      AAG42365 standard; Protein; 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            understanding the interaction of a protein with other molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Column 375-376; 113pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 SNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGAN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDNRGVFIICNYEPRGNIAGMKPY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFWGSAGFDWKAVDAVRSWYDEKQWYNYATNSCAAGKVCGHYTQVVWRATTSIGCARVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SENSPODYLTPONSARAAVGVGPVTWSTKLQQFAEKYAAQ--RAGDCRLOHSG-GPYGEN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATG-ATLTLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGW--ASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-0857224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299; DB 20;
No. 4.4e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 141;
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                                                                                              pathway;
promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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222-JUL-1 223-JUL-1 23-JUL-1 23-JUL-1 23-JUL-1 23-JUL-1 23-JUL-1 27-JUL-1 27-JUL-1 28-JUL-1 27-JUL-1 28-JUL-1 29-JUL-1 2	13-JUL-1 14-JUL-1 15-JUL-1 16-JUL-1 19-JUL-1 19-JUL-1 19-JUL-1 19-JUL-1 19-JUL-1 20-JUL-1 20-JUL-1 20-JUL-1 21-JUL-1
	13-JUL-1999 14-JUL-1999 15-JUL-1999 16-JUL-1999 16-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 20-JUL-1999 20-JUL-1999 21-JUL-1999 21-JUL-1999 21-JUL-1999 21-JUL-1999 21-JUL-1999 21-JUL-1999
22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 24-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 28-JUL-1999; 29-JUL-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 21-AUG-1999; 21-AU	13-JUL-1999; 14-JUL-1999; 15-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 20-JUL-1999; 20-JUL-1999; 20-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999;
22-JUL-1999 22-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 24-JUL-1999 25-JUL-1999 26-JUL-1999 27-JUL-1999 27-JUL-1999 28-JUL-1999 29-JUL-1999 29-JUL	13-JUL-1999 99US 14-JUL-1999 99US 15-JUL-1999 99US 16-JUL-1999 99US 19-JUL-1999 99US 19-JUL-1999 99US 19-JUL-1999 99US 19-JUL-1999 99US 19-JUL-1999 99US 19-JUL-1999 99US 20-JUL-1999 99US 20-JUL-1999 99US 21-JUL-1999 99US
22-JUL-1999; 99US-01. 22-JUL-1999; 99US-01. 23-JUL-1999; 99US-01. 23-JUL-1999; 99US-01. 23-JUL-1999; 99US-01. 23-JUL-1999; 99US-01. 24-JUL-1999; 99US-01. 25-JUL-1999; 99US-01. 26-JUL-1999; 99US-01. 27-JUL-1999; 99US-01. 28-JUL-1999; 99US-01. 29-JUL-1999; 99US-01.	13-JUL-1999; 99US-01- 14-JUL-1999; 99US-01- 15-JUL-1999; 99US-01- 16-JUL-1999; 99US-01- 16-JUL-1999; 99US-01- 19-JUL-1999; 99US-01- 19-JUL-1999; 99US-01- 19-JUL-1999; 99US-01- 19-JUL-1999; 99US-01- 19-JUL-1999; 99US-01- 20-JUL-1999; 99US-01- 20-JUL-1999; 99US-01- 20-JUL-1999; 99US-01- 21-JUL-1999; 99US-01-
22-JUL-1999; 99US-0145087 22-JUL-1999; 99US-0145089 23-JUL-1999; 99US-0145089 23-JUL-1999; 99US-0145218 23-JUL-1999; 99US-0145218 23-JUL-1999; 99US-0145218 23-JUL-1999; 99US-0145018 27-JUL-1999; 99US-0145018 27-JUL-1999; 99US-0146388 02-AUG-1999; 99US-0147038 04-AUG-1999; 99US-0147038 04-AUG-1999; 99US-01477192 05-AUG-1999; 99US-01477192 05-AUG-1999; 99US-01477192 05-AUG-1999; 99US-01477192 06-AUG-1999; 99US-01477192 07-AUG-1999; 99US-01477192 08-AUG-1999; 99US-01477192 09-AUG-1999; 99US-01477192 11-AUG-1999; 99US-014884171 11-AUG-1999; 99US-0148871 11-AUG-1999; 99US-0148871 11-AUG-1999; 99US-0148872 20-AUG-1999; 99US-0149752 20-AUG-1999; 99US-0149752 20-AUG-1999; 99US-0149752 20-AUG-1999; 99US-0151065 27-AUG-1999; 99US-	13-JUL-1999; 99US-01- 14-JUL-1999; 99US-01- 15-JUL-1999; 99US-01- 16-JUL-1999; 99US-01- 16-JUL-1999; 99US-01- 19-JUL-1999; 99US-01- 19-JUL-1999; 99US-01- 19-JUL-1999; 99US-01- 19-JUL-1999; 99US-01- 19-JUL-1999; 99US-01- 20-JUL-1999; 99US-01- 20-JUL-1999; 99US-01- 20-JUL-1999; 99US-01- 21-JUL-1999; 99US-01-
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                                                                                      Transgenic plants; disease resistance; chimeric DNA; plant pathogenesis-related protein.
         21-MAR-1990;
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61; Conservative 1
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Search completed: March Job time : 38 secs

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24-MAR-1989;
20-JUN-1989;
                                                                                                                                                                                                                                       This is the plant pathogenesis-related protein (PRP), PR-1c. It confers systemic acquired resistance to plants. The corresp. DNA is used, in a chimeric construct, to produce transgenic plant cells or -tissues with the ability to regenerate into plants which are disease resistant.

See also AAQ06179-81, AAQ06183-86 and AAQ06199-Q06208.
                                                                                                                                                                                                                                                                                                                                                               Disease-resistant transgenic plants - obtd. inducible pathogenesis-related protein from
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Stinson JR,
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GYIVSCNYDPPGNVIGKSPY 138
                                                    WGSGDFLTAAKAVEMWVNEKQYYAHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNG
                                                                   WASYR-ARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATG 183
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89US-0329018.
89US-0368672.
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3%; Pred. No. 8.1e-20;
15; Mismatches 51;
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                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
                                                                                              APPLICANT: Benner, Steven A. TITLE OF INVENTION: Predicti NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 03/25/92
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION: TELEPHONE: (International)
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MEDIUM TYPE: 3.5 inch diskette, 1.4 mb storage
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                                                                                                                                                                                                                                                                                                  119 GGYVVSCNYDPPGNVIGQSPY 139
                                                                                                                                                                                                                                                                                                                    183 GATLTLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS: Dixon, D. C.
AUTHORS: Carr, J. P.
AUTHORS: Klessig, D. F.
AUTHORS: Klessig, D. F.
TITLE: Isolation and nucleotide sequence of cDNA clones for
TITLE: pathogenesis related proteins of Nicotiniana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple MacIntosh OPERATING SYSTEM: MacIntosh 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity les 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Word
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 DYLDAHNTARADVGVEPLTWDNGVAAYAQNYVSQ-----LAADCNLVHSHGQYGENLA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                           QGSGDFMT-AAKAVEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVKCNN 118
                                                                                                                                                                                                                                                                                                                                                                                                      QGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN-- 122
                    Zurich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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none
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46.1%; Pred. No. 3.4e-24;
Live 15; Mismatches 47;
                                                                                                                Predicting Folded Structures of Proteins
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262 2437
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; TITLE: infec
; JOURNAL: Nuc
; VOLUME: 16
; PAGES: 9861
; DATE: 1988
US-07-857-224B-104
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                                                                                                                                                                                                    Sequence 100, Application US/07857224B Patent No. 5958784
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                             APPLICANT: Benner, Steven A TITLE OF INVENTION: Prediction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                     181 ATG-ATLTLCLYNPHGNVQGQSPY 203
                                                         STREET:
CITY: Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 SNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGAN 122
STATE: none COUNTRY: Switzerland International post code) CH-8092 ZIP: (note: this is an international post code)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Dixon, D. C.
AUTHORS: Carr, J. P.
AUTHORS: Klessig, D. F.
TITLE: Isolation and nucleotide sequence of cDNA clones for the
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FILING DATE: 03/25/92
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                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                    RDNRGVFIICNYEPRGNIAGMKPY 141
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                                                       Zurich
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Pathogenesis related protein; Table 16 Row
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                                                                        Hadlaubstrasse 151
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                                                                                           Steven A. Benner
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; Pred. No. 9.2e-24;
16; Mismatches 61
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262 2437
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RESULT 5
US-08-181-271A-45
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Patent No. 5614395
Patent No. 5614395
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FILING DATE: 0.7.
CLASSIFICATION: 436
CLASSIFICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEPHONE: (International) 41 1 262 2437
TOTREAX: (International) 41 1 262 2437
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: Cutt, J. C.
AUTHORS: Dixon, D. C.
AUTHORS: Carr, J. P.
AUTHORS: Klessig, D. F.
AUTHORS: Klessig, D. F.
TITLE: Isolation and nucleotide sequence of cDNA clones for the
TITLE: pathogenesis related proteins of Nicotiniana tabacum induced by TMV
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OPERATING SYSTEM: MacInto:
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
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ORGANISM: tobacco
FEARURE: Pathogenesis related protein; Table 16 ROW
PUBLICATION INFORMATION:
                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
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                  APPLICANT:
                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGANQG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYLDAHNTARADVGVEPLTWDDQVAAYAQNYASQ-----LAADCNLVHSHGQYGENLA 58
                                                                                                                                                                                                                                                                                                                                                                                                              WGSGDFLTAAKAVEMWVNEKQYYAHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNG 118
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Neuhaus, occ.
                                                              Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                  Duesing, John H. Friedrich, Lesli
                                                                                                                                                                    Alexander, Danny C. Beck, James J.
                                                   Moyer,
                                                                                                                    Goodman,
                                                                                                                                                                                                       Ryals, John A.
                                              Mary B
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                                                                                                                Robert M.
                                                                                                                                 Leslie B.
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,
           NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07 77

FILING DATE: "RIOR **
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FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION VINCEN
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/632,441
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PRIOR APPLICATION NUMBER: US 08/093,301
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PRIOR APPLICATION NUMBER: US 07/768,122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 6-APR-1993 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/305,566
APPLICATION NUMBER: US 07/305,566
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
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                                                                                                            FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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US 08/042,847

US 07/165,667

US 07/937,197

US 08/045,957

S-19825/P1/CGC 1727

US 07/580,431

US 07/848,506

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 13-JAN-94 COMPUTER READABLE FORM: CORRESPONDENCE ADDRESS: COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS ADDRESSEE: Clam --ADDRESSEE: 7 Skyline Drive Uknes, Scott Ward, Eric I Williams, St PatentIn Release #1.0, Version #1.25 Sperison, Christoph Stinson, Jeffrey R. CIBA-GEIGY Corporation Floppy disk Scott J. s, Shericca C.
CHEMICALLY REGULATABLE
DNA SEQUENCES AND USES 106 US/08/181,271A AND ANTI-PATHOGENIC THEREOF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45,
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APPLICANT: Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 168 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
TYPE: amino acid
TOPOLOGY: line
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                                                                                          SOFTWARE: PatentIn Rele
CURRENT APPLICATION DATA:
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                           APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
COMPRESSIONIES TO THE TOTAL OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                              CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                              APPLICATION NUMBER: FILING DATE: 24-MAN
                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       ADDRESSEE: Claa-Claa-Crapeer: 7 Skyline Drive
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FILING DATE:
                APPLICATION NUMBER:
                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 LLVSTLLLFLVI---SHSCR------AQNSQQ------DYLDAHNTARADV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYVVSCNYDPPG
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1 Similarity 36.7%;
69; Conservation
                                                                                                                                                                                           10532
                                                                                                                                                                                                                          New York
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                                                                                                                                                                                                         USA
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                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                           Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
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Moyer, Mary B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harms, Christian
                                                                                                                                                                                                                                                                  CIBA-GEIGY Corporation
                                                              24-MAY-1995
 13-JAN-94
                                                                                                                                                                                                                                                                                                                                                                                 Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Jean-Marc
                08/181,271
                                                                             US/08/449,315
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Pred. No. 2.6e-22;
Pro. Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (919)541-8689 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
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APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
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FILING DATE: 16-JUL-
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                         101 VEMWYDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYVVSCNYDPPG 160
196 NVQGQSPY 203
                                                                             136 VALWVAEGRYYTHANNTCAAGROCGTYTOVVWRNTAEVGCAQASCATGATLTLCLYNPHG 195
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FILING DATE: 8-MAR-1988
                                                                                                                                                                    82 GVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV 135
                                                                                                                                                                                                               13 LLVSTLLLFLVI---SHSCR-----AQNSQQ------DYLDAHNTARADV 48
                                                                                                                                                                                                                                                      22 LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV 81
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Elmer, James Scott REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/425,504 FILING DATE: 20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/042,847 FILING DATE: 6-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                             GVEPLTWDDQVAAYAQNYASQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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16-JUL-1993
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                                                                                                                           -LAADCNLVHSHGQYGENLAEGSGDFMT-AAKA 100
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US-08-444-803-45
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Patent No. 5
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                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
PILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: CIBA-GEIGY Corporation
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APPLICANT:
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                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
                                                                                                                                                               APPLICATION NUMBER: US (FILING DATE: 8-MAR-1988 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 0:
FILING DATE: 21-DEC-1990
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STATE: New York
                                                                                                                                   APPLICATION NUMBER: FILING DATE: 6-APR
 APPLICATION NUMBER:
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5654414
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Friedrich, Les...
-Aman, Robert M.
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Sperison, Christoph
Stinson, Jeffrey R.
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Beck, James J.
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                                                                                                                                   JMBER: US 08/042,847
6-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jean-Marc
                                                                                                US 07/632,441
                                                                                                                                                                                                  US 07/165,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/444,803
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US 07/848,506
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US-08-449-043-45
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Best Local S
Matches 69
                                                                                                                                                                                                                                                                                             Sequence 45, Application US/08449043 Patent No. 5689044
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                            APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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PRIOR APPLICATION UMBER: US 07/329,018
FILLING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER: US 07/368,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 12-APR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 6-MAR-1 PRIOR APPLICATION DATA:
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                                                                                    APPLICANT:
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APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     196 NVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 VEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNINGGYVVSCNYDPPG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 GVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 LLVSTLLLFLVI---SHSCR------AQNSQQ-------DYLDAHNTARADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGATLTLCLYNPHG
                                                                                                                                                                                                                                                                                                                                                                                                      NYRGESPY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVEPLTWDDQVAAYAQNYASQ------LAADCNLVHSHGQYGENLAEGSGDFMT-AAKA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
69; Conserv
                        Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
                                                                                               Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                    Duesing, John H. Friedrich, Leslie Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                            Beck, James
                                                                                                                                                                                                                                         Ryals, John A.
Alexander, Danny C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.4%; score 286; DB 1; 1
36.7%; Pred. No. 2.6e-22;
tive 22; Mismatches 59;
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                                                                                                                                                                                         Leslie B.
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PRIOR APPLICATION NUMBER: US 07/632,441
APPLICATION NUMBER: US 07/632,441
ETLING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 07/632,441
ETLING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION NUMBER: US 07/848,506
ETLING DATE: 6-MAR-1992
PRIOR APPLICATION NUMBER: US 07/68,122
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
PRIOR APPLICATION DATA:
                     NFORMATION FOR SEQ ID NO:
                                                       NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIARRENT AFFEL-
APPLICATION NUMBER: US/U8/4427,
ETLING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PARTON NUMBER: 08/181,271
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US (FILING DATE: 7-SEP-1990 PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 APPLICATION NUMBER: US 0: FILING DATE: 24-MAR-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0: FILING DATE: 20-JUN-1989 PRIOR APPLICATION DATA:
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FILING DATE: 8-MAR-1
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 12-APR-1993
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                                          (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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1-APR-1991
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CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
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; TYPE: amino a ropology: lin ; MOLECULE TYPE: US-08-449-043-45
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APPLICANT: Alexander, Dar
APPLICANT: Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATION OPERATING SYSTEM: PC-DO SOFTWARE: Patentin Relaction DATA:
                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/181,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                 FILING DATE: 13-JAN-
PRIOR APPLICATION DATA:
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CITY: Tarrytown
CITY: New York
TTATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stinson, Jeffrey R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION. DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 NYRGESPY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 VEMWYDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYVVSCNYDDPG 160
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                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 GYAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 LLVSTLLLFLVI---SHSCR-----AQNSQQ------DYLDAHNTARADV 48
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                                                                                                                  APPLICATION NUMBER: US FILING DATE: 1-APR-1991
                                                                                                                                                                          APPLICATION NUMBER: US FILING DATE: 6-NOV-1992
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                                                                            APPLICATION NUMBER:
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                                                              DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alexander, Danny C.
                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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UMBER: US 07/165,667
8-MAR-1988
                                                                                                                                                                                                                                                                                     13-JAN-1994
                                                                                                                                                                                                                                                                                                                                                             31-MAY-95
                                                          OMBER: US 07/305,566
6-FEB-1989
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                                                                                                                                                                                          us 07/937,197
                                                                                                                                                                                                                                                   US 08/093,301
                                                                                                                                    us 07/678,378
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RESULT 10
US-08-455-416-45
                                                                                           Sequence 45, Application US/08455416 Patent No. 5777200 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US 07/
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US 08/
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FILING DATE: 21-ULC...
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
APPLICATION NUMBER: 20-OCT 1989
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US FILING DATE: 6-MAR-1992 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
                                                         APPLICANT:
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APPLICATION NUMBER: 0
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                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                                  136 VALWVAEGRYYTHANNICAAGRQCGTYTQVVWRNTAEVGCAQASCATGATLTLCLYNPHG 195
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TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                       49 GVEPLTWDDQVAAYAQNYASQ------LAADCNLVHSHGQYGENLAEGSGDFMT-AAKA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 LLVSTLLLFLVI---SHSCR------AQNSQQ------DYLDAHNTARADV 48
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Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
                                                     Ryals, John A.
Alexander, Danny C.
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20-JUN-1989
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FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/305,566
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION NUMBER: US 08/042,847
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 07/632,441
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
APPLICATION NUMBER: US 07/768,122
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US (FILING DATE: 7-SEP-1990
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Hawthorne STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Clon Conserve State Orive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                                                                                                                              FILING DATE:
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Neuhaus, Jec
Peorge F
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Stinson, Jeffrey
Uknes, Scott J.
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Meins, Jr., Frederick
Montoya, Alice
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                                                                                                                                                                                              27-SEP-1991
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6-NOV-1992
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N: 800
            IMBER: US 07/329,018
24-MAR-1989
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Jeffrey R.
                                                                                                                                                        US 07/580,431
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RESULT 11
US-08-455-244-45
; Sequence 45, Application US/08455244
. Patent No. 5789214
. Patent No. TYPORMATION:
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Best Local Similarity 36.7%;
Matches 69; Conservative 22
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                        APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 VALMVAEGRYYTHANNTCAAGRQCGTYTQVVMRNTAEVGCAQASCATGATLTLCLINPHG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 GVEPLTWDDQVAAYAQNYASQ------LAADCNLVHSHGQYGENLAEGSGDFMT-AAKA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 GVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 LLVSTLLLFLVI---SHSCR-----AQNSQQ------DYLDAHNTARADV 48
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                                                                                 STATE:
                                                               COUNTRY:
                                                                                                              STREET:
                                                                                                                             ADDRESSEE:
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                                                   10532
                                                                             Hawthorne
New York
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amino acid
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                                                                                                              E: CIBA-GEIGY Corporation 
7 Skyline Drive
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                                                                 USA
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Montoya, Alice
Moyer, Mary B
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Payne, George B.
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3: Floppy disk
IBM PC compatible
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CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC DNA SEQUENCES AND USES THEREOF
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s; Pred. No. 2.6e-22;
22; Mismatches 59;
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                                 Qy
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                                                                        Query Match
Best Local Similarity
Matches 69; Conserv
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PRIOR APPLICATION NAMER: US 07/632,441
PRIOR APPLICATION NAMER: US 07/425.504
FILING DATE: 05 07/425.504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
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FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acid
                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: S-TELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: US 07/848,506
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/093,301 FILING DATE: 16-JUL-1993 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
13 LLVSTLLLFLVI---SHSCR-----AQNSQQ-----
                                 22 LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV 81
                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                   NAME: Elmer, James Scott REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                          Conservative
                                                                                                                                                                                           linear
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20-OCT 1989
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in Release #1.0, Version
                                                                                         26.4%;
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                                                                      %; Score 286; DB 1;
%; Pred. No. 2.6e-22;
22; Mismatches 59;
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  ---DYLDAHNTARADV 48
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RESULT 12 US-08-454-876-45

Patent No. Sequence

APPLICANT:

APPLICANT:

APPLICANT:
APPLICANT:

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566
                             FILING DATE: 6-FEB-1:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 8-MAR-1:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                            FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08
FILING DATE: 16-JUL-1993
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                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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o. 5804693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ward, Eric R.
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Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuhaus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meins, Jr., Frederick Montoya, Alice
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Harms, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Payne, George B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIBA-GEIGY Corporation
                                                                                     6-FEB-1989
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13-MHER: US 08/093,301
                                   8-MAR-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Shericca C.
CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jean-Marc
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                                                  US 07/165,667
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                                                                                                                                                                                                                                                                                                08/181,271
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 US 08/042,847
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                                              GENERAL INFORMATION:
APPLICANT: Ryals,
APPLICANT: Alexande
APPLICANT: Beck, Jz
APPLICANT: Duesing,
                                                                                                                                       Sequence 4
Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 12-APR-1993 ATTORNEY/AGENT INFORMATION:
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                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                 TYPE: ami
TOPOLOGY:
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ELECOMMUNICATION TO THE STATE S-1
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REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                    49
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                                                                                                                                                                                                                                                                                                                                                                                                                     82 GVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LLVSTLLLFLVI---SHSCR------AQNSQQ------
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                                                                                                                                                                                                                                              NYRGESPY 168
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o. 5847258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
                                                                  Alexander, Danny
Beck, James J.
                                                  Duesing,
                                                                                                      Ryals, John A
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24-MAR-1989
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27-SEP-1991
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20-OCT 1989
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                                                John H.
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Pred. No. 2.6e-22;
2; Mismatches 59;
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APPLICANT:

APPLICANT:

STATE: N

10532

ADDRESSEE:

APPLICANT:

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FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (FILING DATE: 6-MAR-1992
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-CCT 1989
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                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08, FILING DATE: 13-JAN-94 APPLICATION NUMBER: US
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                APPLICATION NUMBER: US 07/368,672 FILING DATE: 20-JUN-1989
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                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 7-SEP
                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 27-SE
FILING
                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10532
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 DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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Stinson, Jeffrey R.
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Sperison, Christoph
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Montoya, Alice
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Moyer, Mary B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER: US 07/937,197
6-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1995
                                                                                                                                                     JMBER: US 07/580,431
7-SEP-1990
                                                                                                                                                                                                         27-SEP-1991
 MBER: US 08/045,957
12-APR-1993
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                                                                                                                                                                                                                                                                           US 07/848,506
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                                                                                                                                                                                                                         US 07/768,122
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MOLECULE TYPE: protein US-08-457-364-45
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Best Local Similarity
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REGISTION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S--
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acid
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                                                                                                                                                                       TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                        STREET: 7 Skylin
CITY: Hawthorne
STATE: New York
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                                                                                                                                     ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                       COUNTRY:
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5851766
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                                                                                            USA
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Montoya, Alice
Moyer, Mary B.
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Harms, Christian
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Stinson, Jeffrey R.
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PatentIn Release #1.0,
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                                                                                                                                                                                                                                                               Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                       Robert M.
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                                                                                                                                                                                                                                                                                                                             Jean-Marc
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Pred. No. 2.6e-22;
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   Version #1
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Best Local Similarity
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EILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
EILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
ETILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
ETILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
ETILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
ETILING DATE: 7-SEP-1990
PRIOR APPLICATION NUMBER: US 07/580,431
ETILING DATE: 7-SEP-1990
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  TELEFAX: (919)541-8689
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acid
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APPLICATION NUMBER: U
FILING DATE: 24-MAR-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
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NAME: Elmer, James sactt
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APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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APPLICATION NUMBER: US 07/305,566
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FILING DATE: 16-UUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
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                      82
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REGISTRATION NUMBER: 36,
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                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/045,957 FILING DATE: 12-APR-1993
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FILING DATE: 31-MAY-1995
GVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV 135
                                                    LLVSTLLLFLVI---SHSCR------AQNSQQ------DYLDAHNTARADV 48
                                                                                                                                                                                                                                                      amino acids
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ilarity 36.7%;
Conservative 2
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24-MAR-1989
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gr: s-19825/p1/cgc 1727
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                                                                                                                              22;
                                                                                                                              Score 286; DB 2;
Pred. No. 2.6e-22;
Pred. No. 59;
                                                                                                                                                                Length 168;
                                                                                                                              Indels
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US-08-456-240-45
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
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APPLICANT:
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APPLICATION NUMBER:
FILING DATE: 6-FEB-1
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CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA
                                             PRIOR APPLICATION DATA:
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                                                                                              FILING DATE: 6-FEB-1989 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                   FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
OTITING DATE: 16-JUL-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 7 Skylin
CITY: Hawthorne
STATE: New York
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                                                             FILING DATE:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08,
              APPLICATION NUMBER: US 08/042,847 FILING DATE: 6-APR-1993
                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams, Shericca C.
VENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
VENTION: DNA SEQUENCES AND USES THEREOF
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Friedrich, Lesan
Friedrich, Lesan
Robert M.
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Payne, George B
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                               8-MAR-1988
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/848,506
ETLING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/768,122
ETLING DATE: 27-SEP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
ETLING DATE: 7-SEP-1990
PRIOR APPLICATION NUMBER: US 07/368,672
ETLING DATE: 20-JUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
ETLING DATE: 20-JUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
ETLING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
ETLING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
ETLING DATE: 12-APR-1993
APPORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,1
Search completed: March 19, 2003, 09:37:12 Job time : 16 secs
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EILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: OT 7648 566
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161 NYRGESPY 168
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                                                                                                                                                                                                                                                                                                                                                101 VEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYVVSCNYDPPG 160
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  221153 seqs,
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01 US-10-078-929-202
01 US-110-068-347-4
01 US-110-078-929-86
02 US-110-078-929-86
03 US-110-078-929-84
04 US-110-078-929-94
05 US-110-068-347-10
05 US-10-078-929-92
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Sequence 2, Appli
Sequence 202, App
Sequence 202, Appli
Sequence 4, Appli
Sequence 86, Appli
Sequence 80, Appli
Sequence 81, Appli
Sequence 96, Appli
Sequence 90, Appli
Sequence 97, Appli
Sequence 98, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 11, Appli
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Sequence 13, Appli
Sequence 14, Appli
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Sequence 18, Appli
Sequence 18, Appli
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0983 a C. Path 911 921 935 935 935 935 936 936 936 936 936 936 936 936 936 936		99911191111111111199999999999999999999
2320 2320 cogenesis-Related of otide and Methods of /09/832,320 10 0/195,801 version 4.0 version 4.0	ALIGNMENTS	US-09-944-413-50 US-09-944-903-50 US-09-944-904-50 US-09-944-907-50 US-09-944-907-50 US-09-944-95-50 US-09-944-44-50-50 US-09-944-44-50-50 US-09-944-862-50 US-09-945-015-50 US-09-945-015-60 US-09-945-015-60 US-09-945-0510-60 US-09-905-2913-285 US-09-907-824-285 US-09-907-824-285
e Length 203;		Sequence 50, Appl Sequence 47, Appl Sequence 485, Appl Sequence 285, Appl S
COLOR BOOK CONTOCK OF THE CHIEF OF CROSS OF	ESULT 1 S-09-832-320-2 S-09-832-320-2 S-09-832-320-2 Sequence 2, Application US/09832320 Patent No. US20010049834A1 GEMERAL INFORMATION: APPLICANT: Crane, Edmund H. APPLICANTION: Delay Included and Methods of Use FILE REFERENCE: 35718/214291 CURRENT APPLICATION NUMBER: US/09/832,320 CURRENT FILING DATE: 2001-04-10 PRIOR APPLICATION NUMBER: US 60/195,801 PRIOR FILING DATE: 2000-04-10 NUMBER OF SEQ ID NOS: 3 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 203 TYPE: PRT ORGANISM: Zea mays S-09-832-320-2 Dest Local Similarity 100.0%; Score 1085; DB 10; Length 203 Best Local Similarity 100.0%; Pred. No. 5.5e-85; Matches 203; Conservative 0; Mismatches 0; Indels 0	ESULT 1 S-09-832-320-2 S-09-832-320-2 S-09-832-320-2 S-09-832-320 Patent No. US20010049834A1 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Crane, Edmund H. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Pathogenesis-Related TITLE OF INVENTION: Maize Pathogenesis-Related TITLE OF INVENTION: Moize Pathogenesis-Related TITLE OF INVENTION: Moize Pathogenesis-Related TITLE OF INVENTION: Moize Pathogenesis-Related TITLE OF INVENTION: J8718-714-291 CURRENT FILING DATE: 2001-04-10 CURRENT APPLICATION NUMBER: US/09/832,320 CURRENT APPLICATION NUMBER: US 60/195,801 PRIOR APPLICATION NUMBER: US 60/195,801 PRIOR PILING DATE: 2000-04-10 NUMBER OF SEQ ID NOS: 3 SOFTMARE: FastSEQ for Windows Version 4.0 SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NOS: 3 SOFTMARE: FastSEQ for Windows Version 4.0 SEQ ID NO SEQ ID

RESULT 2 US-09-840-479-13

Sequence 13, Application US/09840479 Patent No. US20010025380A1

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APPLICANT: Weng, Zude

TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in TITLE OF INVENTION: Stress Response

FILE REFERENCE: BB1357 US NA

CURRENT APPLICATION NUMBER: US/10/078,929

CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: 09/566,394

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133042

PRIOR APPLICATION NUMBER: 60/133042

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133427

PRIOR APPLICATION NUMBER: 60/133427

PRIOR APPLICATION NUMBER: 60/133437

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APPLICANT: Crane, Virginia
TITLE OF INVENTION: Family Of Maize PR-1 Genes
FILE REFERENCE: 5718-32, 035718/175219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
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APPLICANT:
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CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/257,583
PRIOR FILING DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 37
PRIOR
PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 ACLLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARA 79
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        APPLICATION NUMBER: FILING DATE: 1999-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWVSEKQYYDHDTNSCAEGQVCGHYTQVVWRDSTAIGCARVVCDNNAGVFIICSYNPPGN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVGVGPVSWDDTVAAYAQSYAAQ--RQGDCQLTHSG-GPYGENLFWGSAGADWSASDAVG
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Thorpe, Catherine
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Sakai, Hajime
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Pred. No. 3.7e-21;
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US-10-068-347-4
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APPLICANT: Pioneer Hi-Bred International,
APPLICANT: Simmons, Carl
                                                                                                                                                                                                                        Matches
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Best Local Similarity
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PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/137667
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/267,052 PRIOR FILING DATE: 2001-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/068,347
CURRENT FILING DATE: 2002-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Maize PR1 Polynucleotides and Methods of Use FILE REFERENCE: 35718/242798 (5718-151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 12
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                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 163
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 171
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                                                                                                           102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 VQGQSPY 203
125
                                  158 QCGTYTQVVWRNTAEVGCAQASCATGA-TLTLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 LWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGA-TLTLCLYNPHGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
                                                                       67 NQ-RAGDCRLVHSG-GPYGENLFWGSAGYAWTASNAVGSWAAEKQYYNHATNTCSAPSGQ 124
                                                                                                                                               17 VVAAAAAAGRVVSAQN------TAQDFVNLHNSPRADVGVGNVAWNTTVA-AYAQSYA 66
                                                                                                                                                                     42 VLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 DVGVGPVSWDDTVAAYAQSYAAQ--RQGDCKLIHSG-GPYGENLFWGSAGADWSASDAVG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 AVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 ACLILATILALCAAPAPTHGARVIMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 39.0 nes 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                         QQRRQGGCAFADVGASPYGANQGW--ASYRARPAEVVALWVAEGRYYTHANNTCAA--GR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVGESPY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACLLALAMAATVVAPC-----
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SCGHYTQLVWRASTAIGCARVVCSNNAGVFIICNYYPPGNVIGQSPY
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Acevedo, Pedro
Crane, Virginia
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                                                                                                                                                                                                                                        27.7%;
41.9%;
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                                                                                                                                                                                                                                        Score 300.5; DB 9 Pred. No. 1.5e-18;
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Pred. No. 3.7e-21;
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                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                        Indels 17;
 171
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Famodu,

Encoding Proteins

Involved

in

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APPLICANY: Thorpe, Catherine
APPLICANY: Weng, Zude
APPLICANY: Weng, Zude
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR PILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR APPLICATION NUMBER: 60/133438
PRIOR APPLICATION NUMBER: 60/133438
PRIOR APPLICATION NUMBER: 60/133438
PRIOR PILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILING DATE: 1999-05-11
PRIOR PILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILING DATE: 1999-05-11
PRIOR PILING DATE: 1999-05-11
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                                                                                                                                                                                                             RESULT 6
US-10-078-929-86
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US-10-078-929-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Zea mays
US-10-078-929-82
   Sequence 86, Application US/10078929
Patent No. US20020152497A1
GENERAL INFORMATION:
APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Guor-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 82
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APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 GCAFADVGASPYGANQGWASYRA-RPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVV 166
                                                                                                                                                                                                                                                                                                                                     119 WRRSTRIGCARVVCADNRGVFIVCSYDPPGNVNGQRPF 156
                                                                                                                                                                                                                                                                                                                                                                                         167 WRNTAEVGCAQASCATG-ATLTLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 AGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
mes 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 DCRLVHSG-GPFGESIFWGAGRAWSAADALRSWVDEKRNYHLSSNTCDPGKVCGHYTQVV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AAAMAAAMMAATASAQN-TPQDFVNLHNRARAADGVGPVAWDARVARYAQDYAA--KRAG 59
Miao, Guo-Hua
Falco, Saverio Carl
Sakai, Hajime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.5%; Score 287; DB 12; 39.9%; Pred. No. 2e-17; tive 23; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Length 164;
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US-10-078-929-86
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PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133438
PRIOR APPLICATION NUMBER: 60/133438
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
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Best Local S
Matches 70
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APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Ca
APPLICANT: Sakai, Hajime
APPLICANT: Famodu, Omolayo C
APPLICANT: Odell, Joan T.
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SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION
APPLICANT: Meyers, Blake
APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved
TITLE OF INVENTION: Stress Response
TILE REFERENCE: BB1357 US NA
CURRENT FALLING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
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TITLE OF INVENTION: Nucleic Acid Fragments
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 NTCDPGKVCGHYTQVVWRXSVRIGCARVVCAANRGVFIT-CNYDPPGNFNGERPF 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 APAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGVAPLRWNAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 ASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASY-RA-RPAEVVALWVAEGRYYTHAN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 70; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 APSKVSLAAVL----AVAISLAMAATTTTSAQNTPQDYVNLHNSARRADGVGPVSWDPKV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT--GATLTLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASFAQSYAA--KRAGDCRLQHSG-GPYGENIFWGSAGRAWSAADAVASWVGEKKNYHYDT
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Thorpe, Catherine
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Joan T.
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40.0%; Pred. No. 2.2e-17;
tive 22; Mismatches 71; Indels 1
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NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 83
LENGTH: 136
TYPE: PRT
ORGANISM: Lycopersicon esculentum
US-10-091-135-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-091-135-83
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TYPE: PRT
; ORGANIZM: Triticum aestivum
US-10-078-929-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILLING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133438
PRIOR APPLICATION NUMBER: 60/133428
PRIOR FILLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR APPLICATION NUMBER: 60/137667
PRIOR APPLICATION NUMBER: 60/137667
PRIOR FILLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/137667
PRIOR FILLING DATE: 1999-05-04
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Matches бі
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SOFTWARE: Microsoft Office 97
SEQ ID NO 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 83, Application US/10091135 publication No. US20030039660A1 GENERAL INFORMATION:
                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/091,135
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 60/272,818
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Spangfort, Michael Dho
TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
FILE REFERENCE: 2313/1H587-US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: King, Te Piao APPLICANT: Spangfort, Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 LCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 ICSYNPPGNYEGVSPY 167
69 EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGAN--QGWA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 APMATACILIATILAICAAPAPTHGARVIMPGGAGAVTKAQQGGTGSGSNATADEYIAPH 74
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les 70; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ADAVQAWVSEKQYYDHGSNSCSAPADKSCLHYTQVVWRDSTAIGCARVVCDGGDGLFI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPAEVVALWVAEGRYYTHANNTCA--AGRQCGTYTQVVWRNTAEVGCAQASCATGATL-T 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAARADVGVGPVTWDDNVA-AYAQNYAEQRR-GDCQLVHSGGQYGENIYGGRGGGADWTA 93
                                                                   tch 24.6%; Score 267; DB 9; al Similarity 44.2%; Pred. No. 8.2e-16; 61; Conservative 13; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.9%; Score 280.5; ilarity 35.7%; Pred. No. 7.3c Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .5; DB 12; Length 167;
7.3e-17;
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                                                                                                                  Length 136;
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                                                                        Indels 10;
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US-10-078-929-84
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PRIOR APPLICATION NUMBER: 09/13038
PRIOR PILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR PILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR PILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR PILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133428
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
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SEQ ID NO 84
LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 84, Application U. Patent No. US20020152497Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/137667
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
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APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
TITLE OF INVENTION: Stress Response
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                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Oryza sativa FEATURE: NAME/KEY: UNSURE LOCATION: (22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                         UNSURE
(150)
UNSURE
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Sakai, Hajime
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TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in TITLE OF INVENTION: Stress Response FILE REFERENCE: BB1357 US NA CURRENT APPLICATION NUMBER: US/10/078,929 CURRENT FILING DATE: 2002-02-19 PRIOR APPLICATION NUMBER: 60/133038 PRIOR FILING DATE: 2000-05-05 PRIOR APPLICATION NUMBER: 60/133038 PRIOR APPLICATION NUMBER: 60/133038 PRIOR APPLICATION NUMBER: 60/133042 PRIOR PILING DATE: 1999-05-07 PRIOR APPLICATION NUMBER: 60/133427 PRIOR FILING DATE: 1999-05-07 PRIOR PILING DATE: 1999-05-07 PRIOR APPLICATION NUMBER: 60/133427 PRIOR APPLICATION NUMBER: 60/133437 PRIOR APPLICATION NUMBER: 60/133437 PRIOR APPLICATION NUMBER: 60/133437 PRIOR APPLICATION NUMBER: 60/133437 PRIOR PILING DATE: 1999-05-11 PRIOR PILING 
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; NAME/KEY: UNSURE
; LOCATION: (163)
US-10-078-929-84
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US-10-078-929-96
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SEQ ID NO 96
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                                                                                      Matches
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Patent No. US20020152497A1
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-05-11
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SOFTWARE: Microsoft Office 97
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|| : :|||: || | :| | | | | | :
124 WRKSVRIGCARVVCAAXRGVEIT-CNYXPRATSTGXRPE 161
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                                                                                         Local Similarity les 53; Conserv
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Odell, Joan T.
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Thorpe, Catherine
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                                                                                         Conservative
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                                                                                      ; Score 255; DB 12;
; Pred. No. 1e-14;
21; Mismatches 60;
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                                                                                         60;
                                                                                                                                            Length 161;
                                                                                      Indels
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CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133428
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US-10-078-929-90
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TYPE: PRT
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PRIOR ETLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-05-11
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161
                                      174 GCAQASCATGATLTLCLYNPHGNVQGQSPY 203
                                                                                  102
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                                                                                                                                                                47 GCIAESLEFLFRHNLVRAAKWELPLMWDFQLEQYARWWAG----ERKADCKLEHSFPED 101
                                                                                                                                                                                              62 GSNATADEYLAPHNQARAAVGVAPLRWNAGLASAA---AGTVAQQRRQGGC----AFADV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 GYGEMKGSDAVKFWLTEKPYYDHYSNACVHD-ECLHYTQIVWRDSVHLGCARAKCNNGWV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 TPQDFLDVHNQARAEVGVGPLSWNHTL-QAYAQRYANERIP-DCNL-EHSMGPFGENLAE
                                                                                                                                                                                                                                                                            Local
                                                                                                           GASPYGANQGWASYRA-RPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTYQVVWRNTAEV 173
GCARVVCDDGDVFMTCNYDPVGNYVGERPY 190
                                                                                  GFK-LGENIYWGSGSAWTPSDAVRAWADEEKYYTYATNTCVPGQMCGHYTQIVWKSTRRI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGAT 185
                                                                                                                                                                                                                                                                                                                                                                                                          190
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58; Conserv
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Thorpe, Catherine
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                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                  23.4%; Score 254; DB 12;
38.7%; Pred. No. 1.5e-14;
ative 18; Mismatches 60
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                                                                                                                                                                                                                                                                                            Length 190;
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RESULT 12 US-10-078-929-94

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CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
PRIOR PILING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR PILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR PILING DATE: 1999-05-11
PRIOR PILING DATE: 1999-05-11
PRIOR PILING DATE: 1999-05-11
PRIOR PILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/13438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/13436
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/137667
PRIOR PILING DATE: 1999-05-13
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US-09-840-479-7
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GENERAL INFORMATION:

GENERAL INFORMATION: Virginia
APPLICANT: CTAME, Virginia
TITLE OF INVENTION: Family Of Maize PR-1 Genes
FILE REFERENCE: 5718-32, 035718/175219
CURRENT APPLICATION NUMBER: U5/09/840,479
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/257,583
                                                                                                                                                                                                                                          Sequence 7, Application US/09840479 Patent No. US20010025380A1
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APPLICANT: Rafalski, Antoni
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Patent No. US200
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APPLICANT:
APPLICANT:
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APPLICANT: Odell, Joan T.
APPLICANT: Meyers, Blake
APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 FVICSYSPPGNIEGERPY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 LTLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 ASYRARPAEVVALWVAEGRYYTHANNTCAAGROCGTYTQVVWRNTAEVGCAQASCATGAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity hes 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 TADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGW 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 TPQDFLDVHNQARAEVGVGPLSWNHTL-QAYAQRYANERIP-DCNL-EHSMGPFGENLAE
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Sakai, Hajime
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320020152497A1
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Pred. No. 3.4e-14;
1; Mismatches 61;
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                                                                                                                                            And Promoters
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; NAME/KEY: UNSURE ; LOCATION: (107)..(108)..(109)..(110) ; NAME/KEY: UNSURE ; LOCATION: (137) US-10-078-929-98
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TITLE OF INVENTION: Nucleic Acid Fragments En
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/13304
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133479
PRIOR PRIOR DATE: 1999-05-11
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; TYPE: PRT
; ORGANISM: Zea mays
US-09-840-479-7
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Best Local S
Matches 53
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NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Office 97 SEQ ID NO 98
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Query Match
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PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
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PRIOR FILING DATE: 1999-05-1
PRIOR APPLICATION NUMBER: 60
PRIOR FILING DATE: 1999-05-1
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PRIOR FILING DATE: 1999-05-1
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                                                                                                                                                                                                                                                                                                                                   ORGANISM: Triticum
                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 SYRA-RPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGA 184
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al Similarity 44.5%;
53; Conservation
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Thorpe, Catherine
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    22.1%;
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Pred. No. 1.9e-13;
    Score 240;
    DB
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    12;
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    Length 156;
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GENERAL INCORPORATION:
GENERAL INCORPORATION:
APPLICANT: Pioneer Hi Bred International, Inc.
APPLICANT: Simmons, Carl
APPLICANT: Simmons, Carl
APPLICANT: Acevedo, Pedro
APPLICANT: Crane, Virginia
TITIE OF INVENTION: Maize PRI Polynucleotides and Methods of Use
FILE REFERENCE: 35718/24798 (5718-151)
CURRENT APPLICATION NUMBER: US/10/068,347
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/267,052
PRIOR APPLICATION NUMBER: 60/267,052
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 12
SOPTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 166
TYPE: PAT
CORGANISM: Zea mays
US-10-068-347-2
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US-10-068-347-2

; Sequence 2, Application US/10068347

; Patent No. US2022166146A1
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Search completed: March 19, 2003, 09:41:47 Job time: 17 secs
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                                                                                                                                                                                       97 AGTVAQQRRQ---GGCAFADVGASPYGAN--QG-----WASYRARPAEVVALWVAEGRYY 146
                                                                                                                                                                                                                                                                        46 GGAGAYTKAQQGGTG-----SGSNATA-DEYLAPHNQARAAYGVAPLRWNAGLASAA 96
                                                                                                                                                                                                                               3 GYGGATGKASSGGGGLDPDGDPEVGLNGKAIEEIVNEHNVFRAKEHVPPLVWNATLA--- 59
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February 22, 2003, 04:06:26; search time 44.5828 Seconds (without alignments) 4209.836 Million cell updates/sec
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/pcrUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/pcrUS_COMB.seq:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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SUMMARIES

Search completed: February 22, 2003, 06:08:15 Job time : 44.5828 secs



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Copyright (c) 1993 - 2003 Compugen Ltd.
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REFERENCE AUTHORS TITLE SOURCE ORGANISM RESULT 1 BE512404 LOCUS FEATURES VERSION KEYWORDS COMMENT ACCESSION DEFINITION JOURNAL source University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences Zea mays. Zea mays Email: walbot@stanford.edu Plate: 946070 row: F column: Location/Qualifiers 400 pm mRNA linear EST 07-AUG-2000 mays cDNA, mRNA sequence.

BE512404 Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 3227 Fax: 650 725 8221 Maize ESTs from various cDNA libraries sequenced at Stanford Walbot, V. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 486) BE512404.1 EST. /organism="Zea mays" GI:9733652 05

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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
BG343299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390;
                                                                      Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex pre-anthesis spike cDNA library
                                                                                                                                                                                                          Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                              BG343299 996 bp mRNA linear EST 22-OCT-HVSMEg0005F16f Hordeum vulgare pre-anthesis spike EST library HVcDNA0008 (white to yellow anther) Hordeum vulgare cDNA clone HVSMEg0005F16f, mRNA sequence.
BG343299 BG343299 1 GI:13155628
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                                                    for barley genomics: Morex Unpublished (2001)
                                     Contact: Wing RA
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                University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 by to 3 Kb with a 1 Kb average."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="OH43"
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98.78;
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                                                                              GCCCCGCTGCGGTGGAGCGCGACCTGACGGCGGCGGCGGCGTGGACCGCGTCGCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 864 656 4293
Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop:
    Location/Qualifier
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864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yellow with awis trimmed were Collected RNA was prepared from each pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close lab (Choi) at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing) Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/projects/barley. To barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

83 a 310 c 377 g 123 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spike with awns trimmed were collected at white, green and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="HVSME90005F16f"
/clone_lib="Hordeum vulgare pre-anthesis spike
HVcDNA0008 (white to yellow anther)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pre-anthesis spike"
/lab_host="SOLR"
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/cultivar="Morex"
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Pred. No. 2.1e-34;
0; Mismatches 111
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Matches 317; Conser
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GGCCCCGCTGCGGTGGAGCGCCGACCTGACGGCGGCGGCGGCGTGGACCGCGTCGCAGCA 60
             GGCCCCGCTGCGGTGGAACGCGGGCCTGCCTTCGGCCGCCGCGGGGACGGTGGCGCAGCA 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vulgare
ENMARYOta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Trittoeae; Hordeum.
1 (bases 1 to 362)
1 (bases 1 to 362)
                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Card Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001)
On Nov 21, 2001 this sequence version replaced gi:17032393. Contact: Waugh R, Marshall DF
                                                                                                                                                                                                                                                                                                                                                                                Seq
                                                                                                                                                                                                                                                                                                                                                                                           Email: est@scri.sari.ac.uk
All sequence has a Phred quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM101325 362 bp mRNA linear EST 23-JUL-2002 EBpi01_SQ003_I13_R pistil, 1 DPA, no treatment, cv Optic, EBpi01 Hordeum vulgare cDNA clone EBpi01_SQ003_I13 5', mRNA sequence.
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EBp101_SQ003_I13_R pistil, 1
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                                                        Conservative
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                                                                                                                 /note-"Vector: pspOrT1; Site_1: Sal I; Site_2: Not I;
/note-"Vector: pspOrT1; Site_1: Sal I; Site_2: Not I;
/non-normalised library, directionally cloned into pspOrT1.
Derived from pistils dissected from developing grains (24 hours post anthesis) in glasshouse grown barley plants.
Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."

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                                                                                                                                                                                                                                                  /clone="EBpi01_SQ003_I13"
/clone=lib="pistil, 1 DPA, no treatment,
/tissue_type="pistil"
/dev_stage="1 DPA"
                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                      'lab_host="DH10B"
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                                                     Score 290; DB 13;
Pred. No. 5.3e-29;
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les 258; Conserv
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CGAACCAGGGGT-GGCAAGCTACCCGGCGCGCGCCCCGCGNAGGTGGTGGCGTCGTGGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaae; Oryza.
1 (bases 1 to 681)
Sasaki, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU082529 Rice panicle shorter than 3cm Oryza sativa (japonica cultivar-group) cDNA clone E30820, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasaki,T. and Yamamoto,K. Rice cDNA from panicle (2 Unpublished (2000)
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AU082529
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Fax: 81-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Takuji Sasaki
National Institute of
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                                                                                                                                                                                                                                                                                                                                                                                                         PROJECT
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: tsasaki@abr.affrc.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice Genome Research Program,
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                                                                                                                                                                                                                             136
                                                                                                                                        Conservative:
                                                                                                                                                                                                                         /db_xref="taxon:39947"
/clone="E30820"
/clone_lib="Rice panicle shorte
/clone_lib="Rice panicle shorte
/dev_stage="shorter than 3cm"
/note="Organ: panicle"
a 187 c 214 g 141 t
                                                                                                                                                                                                                             D
                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa
/cultivar="Nipponbare"
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                                                                                                                                                       23.1%;
                                                                                                                                      Score 207.8;
Pred. No. 1.9e
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Program, Kannondai 2-1-2,
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               CACCCACGCCAACAACACGTGCGCCGCGGGGGGGCGCAGGTGCGCACGTACACGCAGGTGGT 559
                                                             GCGGCGGTGCGGGTTCGCGGACATGAGCGGGA-CCCCTACGGCGCGAACCAGGGGTGGGC 59
                                                                                                                                          GGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGGGC 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | CGTACACGCAGGTGGTGTGGGCGAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCCTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 293)
Sasaki, T. and Yamamoto, K.
Rice CDNA from immature leaf including apical meristem
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU029886 Rice cDNA from immature leaf including apical meristem Arvza sativa (japonica cultivar-group) cDNA clone E50124_lA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: tsasaki@abr.affrc.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institute of Agrobiological Resources Rice Genome Research Program, Kannondai 2-1-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Taku
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                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                  /note="Organ: leaf; immature leaf including meristem (under long day condition)" 102 c 107 g 33 t 2 others
                                                                                                                                                                                                                                                                                                                    meristem"
                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa (japonica cultivar-group)"
| (cultivar="Nipponbare" |
| /db_xref="taxon:39947" |
| /clone="E50124_lA" |
| /clone_1ib="Rice cDNA from immature leaf including apical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Japan
                                                                                                                                                                                                                                                                                                     /dev_stage="immature"
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URL:http://rgp.dna.affrc.go.jp/
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Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine
4.444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #W1252852 500 bp mRNA linear EST 03-MAY-2002 san81q09.y2 Gm-c1052 Glycine max cDNA clone SOYBBAN CLONE ID: Gm-c1052-6090 5' similar to SW:ST14_SOLTU Q41495 STS14 PROTEIN PRECURSOR. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Seq primer: -40RP from Gibco
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Fax: 314 286 1810
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Location/Qualifiers
                        /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The Harrosoy NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from whole seedlings of 1 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments were directionally cloned into the EcoNa fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation
with Dr. Paul Keim's laboratory at Northern Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="1 week old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1052-6090"
/clone_lib="Gm-c1052"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Glycine max"
/db xref="taxon:3847"
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Direct Submission
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project,
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
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AY106735
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Zea mays
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                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 759)
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 /note="this sequence is part of a project assemblies resulting from the application
                                                                  /organism="Zea mays"
/db_xref="MaizeDB:635032"
/db_xref="taxon:4577"
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                                                        /clone="PC0088779"
                                         /clone_lib="Maize Mapping Project/DuPont Cornsensus
                                                                                                                                                                                                                                                                                                                                                                  GI:21209813
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rt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<a href="http://www.tigr.org/softlab/">http://www.tigr.org/softlab/</a>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the
                                                                                                                        Tel: 515-294-0975
Fax: 515-294-2299
                                                                                                                                                 G405 Agronomy,
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Best Local Similarity Matches 258; Conserv
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                     CGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGCCAGAGCCCCTACTAG 674
                                                                              TGTGGCGCGACTCCACCGCCATCGGCTGTGCCCGCGTCGTCTGCGACAACAACGCCGGCG
                                                                                                   TGTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCG---CCACGGGCGCCA 615
                                                                                                                                                        ACACCCACGCCAACAACACGTGCGCCGCGGGGGGGGGCAGTGCGCACGTACACGCAGGTGG
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TCTTCATCATCTGCAGCTACAACCCGCCGGCAACGTCGTCGGCGAGAGCCCCTACTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

a 229 c 210 g 145 t
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Pred. No. 1.6e-09;
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sequence. BM337818 Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages including seedlings treated with a variety of hormones unpublished (2001) Eukaryota; Viridiplantae; Streptophyta; Er Spermatophyta; Magnoliophyta; Liliopsida; MEST217-G08.T3 вм337818 Schnable Laboratory Contact: Patrick S. Schnable clade; Panicoideae; Andropogoneae; Zea mays Zea mays. вм337818.1 State University GI:18167978 631 bp mRNA linear EST 16-JAN-2002 ISUM5-RN Zea mays cDNA clone MEST217-G08 3', mRNA Zea. Embryophyta; Tracheophyta; a; Poales; Poaceae; PACC and tissues

Individual basecall and phred software,

(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b

confidence value were assigned using

the

Email: schnable@iastate.edu

Iowa

Iowa State University,

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TGTGGCGCGACTCCACCGCCATCGGCTGTGCCCGCGTCGTCTGCGACAACAACGCCGGCG
                                           TGTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAGGCAGCTGCG----CCACGGGCGCCA 615
                                                                                               ACGACCACGACACCAACAGCTGCGCGGAGGGGCCAGGTGTGCCGGCCACTACACGCAGGTGG
                                                                                                                                           ACACCCACGCCAACAACACGTGCGCCGCGGGGGGGCGGCAGTGCGCCACGTACACGCAGGTGG 558
                                                                                                                                                                                              CCGGCGCCGACTGGCGTCCGACGCCGTGGGCTCCTGGGTGTCCGAGAAGCAGTACT
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BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT7179AC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."
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/lab_host="DH10B"
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/clone_lib="ISUM5-RN"
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61.1%;
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KEYWORDS
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BG840355
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AUTHORS
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JOURNAL
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                                                                                                                                                                   Matches 254;
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                     Best Local Similarity
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                                                                                                378 CAGGGCGGGTGCGCGTTCGCGGACGTGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGG
                                    166
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                                                               CTGCGGTGGAACGCGGGCCTGGCTTCGGCGGCGCGCGGGGACGGTGGCGCAGCAGCGGCG
                                  GTGGCGTGGGACGCCAGGGTGGCCAGGTACGCGCAGGACTACGCGGCGAAGCGCGCCGGG
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BG840355
BG840355.2
EST.
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G405 Agronomy, Iowa
Tel: 515-294-0975
Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      628 bp mRNA linear EST 29-MAY-2001
MEST12-D09.T7-1 ISUM4-TN Zea mays cDNA clone MEST12-D09 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On May 25, 2001 this sequence version replaced gi:14206677 Contact: Patrick S. Schnable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T7-1 (AA TAC GAC TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                                                                                 ECORI and Notl sites of the PTTTTARC vector. The library then went through one round of normalization to COT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

a 210 c 228 g 92 t
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/lab_host="DH10B"
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/cultivar="B73"
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/clone_lib="ISUM4-TN"
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                                                                                                                                                                       0;
                                                                                                                                                                   Score 133.8; DB 12;
Pred. No. 8.6e-09;
0; Mismatches 157;
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RESULT 10
BG873702/c
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGGCCAGAGCCCCCTAC 671
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Zea mays
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BG873702
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)
Contact: Patrick S. Schnable
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Qiu,F., Cui,F., Guo,L.,
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               113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               State University
       Agronomy, Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                     515-294-0975
                                                                                                                                                                                                                                                                                                                                                                                                                         schnable@iastate.edu
                                                                                                                                                                                                                             /clone_lib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                        /organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
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RESULT 11
BG840318
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AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCGC----CACGGGCGCCC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACTGCCGGCTGCTCCACTCGGGCGGCCGTTCGGCGAGAACATC---TTCTGGGGCCTCG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
BG840318
BG840318.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                            Expressed Sequence Tags from Unpublished (2001) Contact: Patrick S. Schnable
                                                                                                                                                                       FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT, AAC CCT CAC TAA AG)
Seg primer: primer T7-1 (AA TAC GAC TC
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MEST9-A05.T7-1 ISUM4-TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays
                                                                                                                                                                                                                        PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 714)
                                                                                                                                                                                                                                                                                                                                                                            F., Cui, F., Guo, L.,
                                                                                                                                                                                                                                                    515-294-2299
                                                                                                                                                                                                                                                                   Agronomy, To 515-294-0975
                                                                                                                                                                                                                                                                                                State University
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                                                                                                                                                                                                                                     schnable@iastate.edu
/organism="Zea mays"
/oultivar="B73"
/db_xref="taxon:4577"
/clone=!MEST9-A05"
/clone=!ib="ISUM4-TN"
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/tlssue_type="Seedling and silk"
/tlab_host="DH1DB"
/note="Vector: pT7T3PAC; Site_1: Ec
                                                                                                                                                        Location/Qualifiers
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60.9%;
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Pred. No. 8.3e-09;
                                                                                                                                                                                                                                                                                                                                                             from
                                                                                                                                                                                                                                                                                                                                                                          Ashlock, D.A,
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ze Seedlings
                                                                                                                                                                            CTA
      ECORI; Site_2: NotI;
as follows. First-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear EST 29-MAY-2001
e MEST9-A05 5', mRNA
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ngs and Silks
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RESULT 12
BM350281/c
                                                                                                                                                                                                                                                                                                                     KEYWORDS
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                                                                                                                                 JOURNAL
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                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCTTCATCGTCTGCAGCTACGACCCCCCGGGCAACGTCAACGGCCAGCGCCCCGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGTGGCGCAGGTCCACCCGCATCGGCTGCGCGCGGTCGTCTGCGCCGACAACCGCGGC
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                                                                                                                                                                                                                                                                                                                                       вм350281
вм350281.1
                                                                                         Contact: Patrick S. Schnable Schnable Laboratory
                                                                                                                               Unpublished (2001)
                                                                                                                                           Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S Expressed Sequence Tags from B73 Maize: various stages including seedlings treated with a variety of hormones
                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                 EST
Zea
                                                                                                                                                                                                                                                                                                                                                                                               MEST263-E11
                                                                                                                                                                                                                                                                                   Zea mays
                                                                                                                                                                                                       (bases 1 to 719)
                                                                                                                                                                                                                                                                                                   mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                       State University
                     515-294-2299
                                     Agronomy, Iowa
515-294-0975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT7T3PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5'
                                                                                                                                                                                                                                                                                                                                                                                                 .
T3
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                                                     State University, Ames, IA 50011-1010,
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Pred. No. 8e
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                                                                                                                                                                                                                                                                                                                                                                                           mRNA linear EST 16-JAN-2002 CDNA clone MEST263-E11 3', mRNA
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437

540

483

377 600 Qy

318 599

 Query Match Best Local S Matches 254

Similarity

14.9%;

Score 133.8; DB 13; Pred. No. 8e-09; Mismatches

Length

Conservative

0;

157;

6

Gaps

2

hes 254;

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482 438

GACTGCCGGCTGCTGCACTCGGGCGGGCCGTTCGGCGAGAACATC---TTCTGGGGGCTCG

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ORIGIN
                                    BASE COUNT
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Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG) BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG) Seq primer: primer T3 (ATT AAC CCT CAC TAA AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Individual basecall and confidence value were assigned using Phred software,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR PRimers
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                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="MEST263-E11"
/clone_lib="ISUM5-RN"
/tissue_type="mixed"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI; Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels (3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, callus, NAA (a-Naphthalene acetic acid)-treated seedlings,
                                resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT/TJPAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research'6: 791-806, 1996)."
                                                                                                                                                                                                                                                                   resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the
                                                                                                                                                                                                                                         ds-cDNAs were digested with NotI and size-selected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinetin-treated seedlings, ACPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="2ea mays"
/cultivar="B73"
/db_xref="taxon:4577"
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linear EST 19-JUL-2000 Sorghum bicolor cDNA, mRNA

plants

Sudman, M. and Pratt

vector and regions

sequence

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JOURNAL
REFERENCE
AUTHORS
TITLE
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Best Local
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                                                                                                                                                                              GTGGCGTGGGACGCCAGGGTGGCCAGGTACGCGCAGGACTACGCGGCGAAGCGCGCGGG
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Zea mays
AY105799
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coe, E.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
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Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whit
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project Mapping Proje
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC0149775 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="this sequence is part of a project of EST assemblies resulting from the application of public
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="MaizeDB:638840"
/db_xref="taxon:4577"
/clone="PCO149775"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Maize Mapping Project/DuPont Cornsensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:21208877
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                                                                                                                                                                                                                                                                                                                                                            0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 g
                                                                                                                                                                                                                                                                                                                                                                               Score 133.8; DB 1
Pred. No. 7.4e-09;
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                                                                                                                                                                                                                                                                                                                                                            Mismatches 157;
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                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Embryophyta; Tracheophyta;
a; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                     Matches 254;
                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                   CGGCGGACGAGTACCTGGCGCGCACACACCAGGCGGCGCGCGGTGGGCGTGGCCCCGC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCGC----CACGGGCGCC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACACCCACGCCAACAACACGTGCGCCGCGGGGGCGGCAGGTGCGGCACGTACACACGCAGGTG 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACCACCTGAGCAGCAACACCTGCGACCCCGGCAAGGTGTGCGGCCACTACACGCAGGTG 449
GCGACTGCAAGCTGATCCACTCCGGCGGTCCCTACGGCGAGAACATCTTCTGGGGCTCCG 237
                                                                                                                               AGGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGGG 438
                                                                                       TGTCGTGGGACGACGCTGGCC----GCGTACGCGCAGAGCTACGCGGCGCAGCGGCAGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTGGCGCAGGTCCACCCGCATCGGCTGCGCGCGCGTCGTCTGCGCCGACAACCGCGGC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      below Phred quality 16. The is 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
Sequences have been tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An EST database from Sorghum: water-stressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clade; Panicoideae; Andropogoneae;
1 (bases 1 to 539)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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WS1_1_B04.b1_A002 Water-stressed 1
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                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                        /Clone_lib="Water stressed 1 (WS1)"
/note="lorgan: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
177; c. 182 g 83 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                        Score 132.6; DB 1
Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                     Mismatches 159;
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(WS1)
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Indels Length

2

539; 6; Gaps

Ωy 밁 $Q_{\mathbf{y}}$ 망 Qy

밁 Qy Вp

DB 10;

Length

539;

2

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BASE COUNT
ORIGIN
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BE367566/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTGGCGTGACTCCACGGCCATCGGCTGCGCCCCGCGTCGTCTGCGACAACAACGCCGGCG
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Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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EST.
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An EST database from Sorghum: pathogen-induced plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M.
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706 583 0210
                                   89
                                                                                                                                                                                                                                                  /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Pathogen induced 1 (PI1)"
/clone_lib="Pathogen induced 1 (PI1)"
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: ECORI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is asorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
                                   ۵
                                                                                                                                                                     grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be
                                                                            sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                   pathogen."
173 c 1
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                              TCTTCATCATCTGCAGCTACAACCCGCCGGCAACTACGTCGGCCAGAGCCCATACTAG
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Search completed: March 18, Job time: 1855 secs

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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-08-440-856A-9
US-09-128-155-16
US-08-444-803-11
US-08-444-803-11
US-08-445-265A-11
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Patent No. 6429362
GENERAL INFORMATION:
APPLICANY: Crane, Virginia
TITLE OF INVENTION: Family Of Maize PR-1 Genes
FILE REFERENCE: 5718-32, 035718/175219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Zea mays
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CGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGGCCAGAGCCCCTACTAG
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); Mismatches
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Pred. No. 1.7e-16;
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APPLICANT: Crane, Virginia
APPLICANT: Crane, Virginia
TITLE OF INVENTION: Family Of Maize PR-1 Genes
FILE REFERENCE: 5718-32, 035718/175219
CURRENT FILLYG DATE: 1999-02-25
CURRENT FILLYG DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 37
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SEQ ID NO 6
LENGTH: 866
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Best Local Similarity
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                                                                                 GENERAL INFORMATION:
                                                                                                Sequence 14, Application US/09257583A Patent No. 6429362
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                                      APPLICANT: Crane, Virginia
TITLE OF INVENTION: Family Of Maize PR-1 Genes
FILE REFERENCE: 5718-32, 035718/175219
CURRENT APPLICATION NUMBER: US/09/257,583A CURRENT FILING DATE: 1999-02-25 NUMBER OF SEQ ID NOS: 37
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US-08-440-856A-9
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                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08440856A Patent No. 5750873
GENERAL INFORMATION:
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                                                                                                                                                                                                                                              APPLICANT: DELLAPOR TITLE OF INVENTION:
                                              CURRENT APPLICATION DATA:
                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                          498
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                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                 APPLICATION NUMBER: FILING DATE: 15-MA
                                                                                                   MEDIUM TYPE:
                                                                                                                                   ZIP:
                                                                                                                                              COUNTRY:
                                                                                                                                                             STATE:
                                                                                                                                                                           CITY: WASHINGTON
                                                                                                                                                                                       STREET:
     CLASSIFICATION:
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20037 D.C

Floppy disk

15-MAY-1995

US/08/440,856A

Version

#1.25

USA

2000 PENNSYLVANIA AVE.

DELLAPORTA,

A, STEPHEN L.

MATERIALS AND METHODS FOR PRODUCING PLANTS WITH SINGLE-SEX FLOWERS

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US-09-257-583-14
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: (775)
OTHER INFORMATION: TOTHER INFORMATION: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver.
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LOCATION: (42)..(686)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                              318 CTGCGGTGGAACGCGGGCCTGGCTTCGGCGGCGCGCGGGACGGTGGCGCAGCAGCGGCGG 377
                                                                                                                                                                                                                                                                                           Local Similarity
nes 254; Conserv
                                                            GTGTGGCGCA--ACACCGCCGAGGTCGGGTGCGCGCGAGGCCAGCTGCGC---CACGGGCG
                                                                                                         GACTGCCGGCTGGTGCACTCGGGG ---GGGCCGTTCGGCGAGAGCATCTTCTGGGGCTCG
GCGTCTTCATCGTCTGCAGCTACGACCCCCCGGGCAACGTCAACGGCCAGCGCCCGTTC
              CCACGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGCCAGAGCCCCTAC
                                                                                                                                           CAGGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCAGCCCCTACGGCGCGCGAACCAGGGGTGG
                                              GTGTGGCGCAGGTGTCCACCCGCATCGGCTGCGCGCGTCGTCTGCGCCGACAACCGCG
                                                                                             TACCACCTGAGCAGCAACACCTGCGACCCCGGCAAGGTGTGCGGCCACTACACGCAGGTG
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Pred.
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ATTORNEY/AGENT INFORMATION: NAME: MILLMAN, ROBERT A

REFERENCE/DOCKET NUMBER:

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Sequence 1, Application US/07945283
Patent No. 5352596
GENERAL INFORMATION:
APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 887-1517
                                                                                                                                                                                                                                                                   588 AACGCGCTGGGCGCCGCTC 608
                                                                                                                                                                                                                                                                                  600 TGCGCCACGGGGGGCGCCACGCTC 620
                                                                                                                                                                                                                                                                                                                                                                                  468 CGCSRYGRCGGSCGSCTSGACGTSYWSTGCAACAACGCCGGGGTGCTGGGCCGCCAGACG
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REGISTRATION NUMBER: 36,217
                                                                                                                                                                                                                                                                                                                          CGCGCGGCCARGAGCATCCTGTCSTTCGACGCSGSSGAGTTCGACCGCGTGCTCCGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                              GTGGCGGAGGGGCGGTACTACACCCACGCCAACAACACGTGCGCCGCGGGGGGGCGCAGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGATCGGSGAGGCSATCGTGMGGCTGTTCGYYAAGCACGGGGCCMRGGTGGTGATCGCG
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38.3%; Prer
                                                                                           Pseudorabies Virus Deletion Mutants
Involving The EPO and LLT Genes
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Pred. No. 4.6e-05;
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US-07-945-283-1
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Best Local Similarity 49.8
262; Conservative
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                            4214 GTGCTGGAGCCGGACTTGGTGCTGGCGGGGCTGGAGGCCCGGAGCCCGGAGGCCGGAG
                                                                                                                                                                                                                4038
                                                                                                                                                      4094
                                                                                                                                                                                                                                                                    3978 AGCGGCGCTTGCGCCGGGCCCCCGGTCCTCTTCGTCGTCGCGGTGGCCGTGGCCGTCCC 4037
                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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HYPOTHETICAL: N
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NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
                                                                                                                                                                                                                                              148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                              327
                                                                                                                        267
                                                                                                                                                                                   208
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LOCATION:
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TOPOLOGY: linear
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CLASSIFICATION: 424
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                          GAGTACCTGGCGCGCACAACCAGGCGCGCGCGGCGGTGGGCGTGGCCCCGCTGCGGTGG 326
                                                                                                                                                                    CGCGGAGGGCCGAGCCGGAG----AGCCCCTCGTCCTCCTCGCCGTCCCCGGGGGCGGCGG 4093
                                                                                                                                                                                                                                   TGCGCGTTCGCGGACGTGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGGGCGAGCTAC 446
                                                          GGGGAGCTGGCGTAGCCGGAGGAGCCGGAGGAGGCCGGACTTGGTGCCGGAGCTGGACTTG 4213
                                                                                                                                                NUCLEIC ACID
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49.8%;
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228 240 망

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185 108 ; TOPOLOGY: 1: ; MOLECULE TYPE: US-08-440-856A-9

STRANDEDNESS:

linear CDNA

nucleic acid

LENGTH:

1288 base pairs

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

TELEFAX:

(202) 887-0763

706141

Matches Query Match Best Local :

192;

Conservative

Local Similarity

US-07-945-283-1

TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:

STATE:

Peoria

Вb Qγ 밁 Qy 밁 Š 뫄 Q 뫄

528

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4274

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GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Pan, Yang
TITLE OF INVENTION: MOVEL MOLECULES OF TANGO-77 RE
FILE REFERENCE: 09404/052001
CURRENT APPLICATION UNMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER APPLICATION NUMBER: US 60/054,646
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US-09-128-155-16/c
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Best Local
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                                                                                                                                                                                                                                                                                                                       22264
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                 22204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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500 CACCCACGCCAACACACGTGCGCCGCGGGGCGGCAGTGCGCACGTACACGCAGGTGGT
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hes 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGGCCCCGGCCACGTTGGCCGGGGCGAAGAGGGCCGCCGCGTAGGTCCAGGCGGCCTCG
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                                                                                                                          CGCAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCGCCACGG
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                                                                                                Similarity
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nilarity 47.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No. 0.00039;
0; Mismatches 235
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US-08-181-271A-11
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Patent No. 5
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                                                                                                                                                                                                                                            FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 01
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 8-MAR-1
                                                                                                                                                                                               APPLICATION NUMBER: US 0//6/0,000
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/305,566
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
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                                         PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                      APPLICATION NUMBER: FILING DATE: 21-DE
                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 6-FEB
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 13-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
            APPLICATION NUMBER: US 0 FILING DATE: 20-OCT 1989
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Ward, Eric R.
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Stinson, Jeffrey R.
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Sperison, Christoph
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Meins, Jr., Frederick
Montoya, Alice
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Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goodman,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHEMICALLY REC
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Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             John
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                                                                                                                                                            US 07/165,667
                                                                       US 07/632,441
                                                                                                                  US 08/042,847
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APPLICATION NUMBER:

US 07/768,122

US 07/848,506

APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 6-MAR-

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Patent No. 5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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                                        APPLICANT
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REGISTRATION NUMBER: 36,
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Moye...
Neuhaus, Jean ...
Payne, George B.
Payne, Christoph
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                                                                                                                                                                                                                                                                 Friedrich, Leslie B. Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                                           Alexander, Danny C. Beck, James J.
                                                                                                                                  Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                            Harms, Christian
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7-SEP-1990
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56.28;
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Pred. No. 0.0015;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                   FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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TELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8614
                                                                                                                                       FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/632,441 FILING DATE: 21-DEC-1990
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                 REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
                                                  NAME: Elmer, James Scott REGISTRATION NUMBER: 36,
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VENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC VENTION: DNA SEQUENCES AND USES THEREOF EQUENCES: 106
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20-JUN-1989
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6-MAR-1992
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                                                                                                                         US 08/045,957
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Best Local Similarity
Matches 122; Conserv
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                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                               APPLICATION NUMBER: US/08/444,803 FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                STREET: 7 Skyli:
CITY: Hawthorne
STATE: New York
                                   CLASSIFICATION:
                                                                                                                                                                                                                                  ADDRESSEE: Clba CL-Comparer: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                             COUNTRY:
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Friedrich, Lesa...
Friedrich, Lesa...
Friedrich, Lesa...
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Stinson, Jeffrey R.
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Sperison, Christoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meins, Jr., Frederick
Montoya, Alice
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7.56.2%;
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CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
106
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h, Leslie B.
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08/181,271
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Pred. No. 0.0015;
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                                                                                                #1.25
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; TOPOLOGY: linear; MOLECULE TYPE: cDNA
US-08-444-803-11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
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APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
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APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 07/165,667
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                                    577
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                                                                                                                                                                457 CCGCCGAGGTGGCGCTGTGGGGTGGCGGAGGGGGGGGGTACTACACCCCACGCCAACAACA 516
 439
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APPLICATION NUMBER: US
FILING DATE: 16-JUL-199
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 696 base pairs
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GTGTTGGATGTGCTAGGGTTCAGTGTAACAATGGAGGATATATTGTCTCTTGCAACTATG 498
                                 AGGTCGGGTGCGCGAGGCCAGCTGCGCCACGGGCGCCACGCTCACGCTCTGCCTGTACA 636
                                                                                        CGTGCGCCGCGGGCGGCAGTGCGGCACGTACACGCCAGTGGTGTGGCGCAACACACCGCCG 576
                                                                                                                                        CCGCTAAGGCCGTCGAGATGTGGGTCAATGAGAAACAGTATTATGCCCCACGACTCAAACA 378
                                                                    CTTGTGCCCAAGGACAGGTGTGTGGACACTATACTCAGGTGGTTTGGCGTAACTCGGTTC 438
                                                                                                                                                                                                                  122;
                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: US 07/329,018
24-MAR-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US 08/045,957
12-APR-1993
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                                                                                                                                                                                                                               Score 65; DB 1;
Pred. No. 0.0015;
                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                95;
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                                                                                                                                                                                                              Indels
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RESULT 10
US-08-449-043-11
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GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                          FILING DATE: 6-FEB-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                  APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-APR-1991 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US,
FILING DATE: 24-MAY-19
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                            PRIOR APPLICATION DATA:
                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/093,301 FILING DATE: 16-JUL-1993
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08, FILING DATE: 13-JAN-94
APPLICATION NUMBER:
FTT.ING DATE: 20-OCT
                                            FILING DATE:
                                                        APPLICATION NUMBER:
                                                                                    FILING DATE:
                                                                                                  APPLICATION NUMBER:
                                                                                                                             APPLICATION NUMBER: US 07/165,667 FILING DATE: 8-MAR-1988
                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T: Williams, Shericca C.
INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08449043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ward,
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Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meins, Jr., Frederick Montoya, Alice Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alexander, Danny C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIBA-GEIGY Corporation
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6-NOV-1992
                                                                                   JMBER: US 08/042,847
6-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            John A.
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 US 07/425,504
1989
                                                      US 07/632,441
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RESULT 11
US-08-456-265A-11
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Patent No. 5
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                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Alexan
APPLICANT: Ryals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (919)5
INFORMATION FOR SEQ
                                                                             APPLICANT: Goodman, Robert M.
APPLICANT: Stinson, Jeffrey R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE
TITLE OF INVENTION: DNA SEQUENCES AND USES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
          STREET: 520 man.
CITY: Tarrytown
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 CCGCTAAGGCCGTCGAGATGTGGGTCAATGAGAAACAGTATTATGCCCACGACTCAAACA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 CCGCCGAGGTGGCGCTGTGGGGTGGCGGAGGGGGCGGTACTACACCCCACGCCAACAACA 516
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hes 122;
COUNTRY: USA
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                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTGCGCCGGGGGGGGGAGTGCGGCACACGCAGGTGGTGTGGCGCAACACACCGCCG 576
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5767369
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22; Conservative
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                                              E: CIBA-GEIGY Corporation 520 White Plains Road, P.O.
                                                                                                                                                                                     Alexander, Danny C.
Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : (919)541-8614
(919)541-8689
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20-JUN-1989
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56.2%;
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Pred. No.
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                                                Box 2005
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US-08-456-265A-11
                Query Match
Best Local Similarity
                                                                                                                                                                             NFORMATION FOR SEQ ID NO:
                                                                                                                                                         SEQUENCE CHARACTERISTICS
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                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 24-MAR-1989 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US (FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US (FILING DATE: 6-MAR-1992
                                                                                       TOPOLOGY:
                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/045,957 FILING DATE: 12-APR-1993
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                                                                                                                                          LENGTH:
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                                                                                                                      nucleic acid
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27-SEP-1991
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20-OCT 1989
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7.2%;
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                                                                                                                                                                                                                                                               38,241
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Score 65;
Pred. No.
DB 1;
0.0015;
              Length 696;
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RESULT 12
US-08-455-416-11
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Patent No. 5777200
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                     SOFTWARE: PatentIn Relicurrent APPLICATION DATA:
             PRIOR APPLICATION DATA:
                                                        PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICATION NUMBER: 08,
                                                                                                                              FILING DATE: 13-JAN APPLICATION NUMBER:
                           APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-APR-1991
                                                                       FILING DATE:
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APPLICATION NUMBER:
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Stinson, Jeffrey
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Payne, George B.
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Moyer, Mary B
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Ward, Eric
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Meins, Jr., Fred
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                                                                                                                UMBER: US 08/093,301
16-JUL-1993
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CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
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Jeffrey R.
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US 07/305,566
                                                                                     US 07/937,197
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RESULT 13
US-08-455-244-11
; Sequence 11, Application US/08455244
; Patent No. 5789214
. GENERAL INFORMATION:
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Best Local Similarity 56.3
Matches 122; Conservative
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FILING DATE: 6-APR-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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LENGTH: 696 base pairs
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FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
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27-SEP-1991
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Pred. No. 0.0015;
0; Mismatches 95;
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PRIOR APPLICATION NOMBER: US 07/632,441
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-CCT 1989
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APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
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                                            APPLICATION NUMBER: US 0//540,,,,

FILING DATE: 6-MAR-1992

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 07/768,122
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APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
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APPLICATION NUMBER:
FILING DATE: 1-APR-1
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APPLICATION NUMBER: US,
FILING DATE: 31-MAY-19
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
               FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
                                                                                                                          APPLICATION NUMBER: FILING DATE: 20-OCT PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 16-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/937,197 FILING DATE: 6-NOV-1992
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APPLICATION NUMBER:
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7 Skyline Drive
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Stinson, Jeffrey R.
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Payne, George B.
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Moyer, Mary B.
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Friedrich,
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Alexander, Danny C.
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US 07/580,431
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FILING DATE:

7-SEP-1990

APPLICATION DATA:

US 07/368,672

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                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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LENGTH: 696 base pairs
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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                            NUMBER OF SEQUENCES: 1
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                                                         TITLE OF INVENTION:
                                                                                                                      APPLICANT
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REGISTRATION NUMBER: 36,
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STREET:
               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGTTGGATGTGCTAGGGTTCAGTGTAACAATGGAGGATATATTGTCTCTTGCAACTATG 498
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(919)541-8689
7 Skyline Drive
                                          UKHER, .....
WAITH, ETIC R.
WILLIAMS, Shericca C.
WILLIAMS, Shericca C.
VENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
VENTION: CHEMICALLY REGULATABLE THEREOF
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                                                                                                                     Uknes,
                                                                                                                                   Sperison, Christoph
Stinson, Jeffrey R.
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Moyer, Mary B.
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                                                                                                                                                                                                                                                                        Friedrich,
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                                                                                                                                                                                                                                                                                                                 Alexander, Danny C.
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                                                                                                                                                                 Payne, George B.
                                                                                                                                                                                                                            Meins, Jr., Frederick
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                                                                                                                                                                                   Neuhaus,
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               CIBA-GEIGY Corporation
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                                                                                                                     Scott J.
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                                                                                                                                                                                 Jean-Marc
                                                                                                                                                                                                                 Alice
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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; MOLECULE TYPE: US-08-454-876-11
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APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (
FILING DATE: 1-APR-1991
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                             FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                    FILING DATE: 24-MAR-1989 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                    REGISTRATION NUMBER: 36,129
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/580,431 FILING DATE: 7-SEP-1990
                                   TOPOLOGY:
                                                  STRANDEDNESS:
                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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                                                                                    696 base pairs
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6-MAR-1992
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8-MAR-1988
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Query Match

7.2%;

Score

65; DB 1;

Length 696;

56.2%;

APPLICATION NUMBER:

US 07/305,566

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Ryals,
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,364
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CITY: H
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                                                                                                                                    APPLICATION NUMBER: 08
FILING DATE: 13-JAN-94
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Stinson, Jeffrey R.
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Meins, Jr., Fred
Montoya, Alice
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CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
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Best Local Similarity
Matches 122; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Elmer, James 36,129
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
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APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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APPLICATION NUMBER:
FILING DATE: 7-SEP-1
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LENGTH: 696 base pairs
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499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/425,504 FILING DATE: 20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 6-MAR
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ATCCTCCAGGTAATGTTATAGGCAAAAGCCCATACTA 535
                                ACCCGCACGGCAACGTGCAGGGCCAGAGCCCCTACTA 673
                                                                        GTGTTGGATGTGCTAGGGTTCAGTGTAACAATGGAGGATATATTGTCTCTTGCAACTATG
                                                                                                           AGGTCGGGTGCGCGAGGCCAGCTGCGCCACGCCCACGCTCACGCTCTGCCTGTACA 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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7-SEP-1990
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6-MAR-1992
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21-DEC-1990
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8-MAR-1988
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56.28;
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Pred. No. 0.0015;
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Search completed: March 18, 2003, Job time: 143 secs

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Minimum DB :
Maximum DB :
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Maximum Match 100%
Listing first 45 summaries
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is derived by analysis of the total score distribution.
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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//gn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
//gn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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//gn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
//gn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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CTCGCAC	ESULT 1 S-09-832-320-1 S-09-832-320-1 S-09-832-320-1 S-09-832-320-1 GEMERAL INFORMATION: APPLICANT: Crane, Edmund H. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Path TITLE OF INVENTION: Polynucle FILE REFERENCE: 35718/214291 CURRENT APPLICATION NUMBER: US G CURRENT FILING DATE: 2000-04-10 NUMBER OF SEO ID NOS: 3 SOFTWARE: FASTSEQ for Windows SOFTWARE: FASTSEQ for Windows SEQ ID NO 1 LENGTH: 898 TYPE: DNA ORGANISM: Zea mays FEATURE: NAME/KEY: CDS LOCATION: (63)(674) S-09-832-320-1 OUCLY Match Best Local Similarity 100.0%; Matches 898; Conservative		600.44 601.66 600.44 601.66 600.44 601.66 600.44
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Sequence 3, Application US/09832320

Patent No. US20010049834A1

GENERAL INFORMATION:

APPLICANT: Crane, Edmund H.

APPLICANT: Crane, Virginia C.

ITILE OF INVENTION: Maize Pathogenesis-Related

TITLE OF INVENTION: Polynacleotide and Methods of

FILE REFERENCE: 35718/214291

CURRENT APPLICATION NUMBER: US/09/832,320

CURRENT FILING DATE: 2001-04-10

PRIOR APPLICATION NUMBER: US 60/195,801

PRIOR APPLICATION NUMBER: US 60/195,801

PRIOR FILING DATE: 2000-04-10

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0

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LENGTH: 612
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                                            ORGANISM: Zea
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                                                                                                                                                                                                    Sequence 12, Application US/09840479 Patent No. US20010025380A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 612; Conserv
                                                                                NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 12
LENGTH: 749
                   NAME/KEY: CDS
LOCATION: (92)..(583)
-09-840-479-12
                                                                                                                           TITLE OF INVENTION: Family Of Maize PR-1 Genes FILE REFERENCE: 5718-32, 035718/175219
CURRENT APPLICATION NUMBER: US/09/840,479
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/257,583
PRIOR FILING DATE: 1999-02-25
                                                                                                                                                                                             APPLICANT: Crane, Virginia
                                                 TYPE: DNA
ORGANISM: Zea
FEATURE:
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Pred. No. 3.7e-101;
Score 139;
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Query Match

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PRIOR FILING DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09840479 Patent No. US20010025380A1 GENERAL INFORMATION:
                                                                                                                                                                                                             Query Match 15.3
Best Local Similarity 62.4
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Crane, Virginia
TITLE OF INVENTION: Family Of Maize PR-1 Genes And Promoters
FILE REFERENCE: 5718-32, 035718/175219
CURRENT APPLICATION NUMBER: US/09/840,479
CURRENT FILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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319
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Pred. No. 2.4e-16;
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0; Mismatches 155;
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (760)
US-10-078-929-81
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US-10-078-929-81
US-10-078-929-81; Sequence 81, Application US/10078929; Patent No. US20020152497A1
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PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
Query Match
Best Local Similarity
Matches 254; Conserv
                                                                                                                                                                                      SEQ ID NO 81
LENGTH: 783
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APPLICANT:
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                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/137667
PRIOR FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/078, CURRENT FILING DATE: 2002-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Nucleic Acid Fragments
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
                                                                                                                                                                                                                         SOFTWARE: Microsoft Office
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60, PRIOR FILING DATE: 1999-05-11
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60
PRIOR FILING DATE: 1999-05-1
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/133428 PRIOR FILING DATE: 1999-05-11
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APPLICANT: Miao, Guo-Hua
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                                                                                                                                                    TYPE: DNA
ORGANISM: Zea mays
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Sakai, Hajime
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Thorpe, Catherine
Weng, Zude
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       Conservative
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                          13.6%;
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       0; Mismatches 157;
                        Score 121.8;
Pred. No. 1.6
                      1.6e-13;
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                                         DB 12;
     Indels
                                       Length
     8;
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US-09-840-479-14
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Best Local S
Matches 254
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SEQ ID NO 14
LENGTH: 806
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APPLICANT: Crane, Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application UP Patent No. US20010025380A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Family Of Maize PR-1 Genes FILE REFERENCE: 5718-32, 035718/175219 CURRENT APPLICATION NUMBER: US/09/840,479 CURRENT FILING DATE: 2001-04-23 PRIOR APPLICATION NUMBER: 09/257,583 PRIOR FILING DATE: 1999-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure LOCATION: (775)
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                              LOCATION: (42)..(686)
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            CTGCGGTGGAACGCGGGCCTTGGCTTCGGCGGCGCGCGGGGGACGGTGGCGCAGCAGCAGCGGGG
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                                                                            CAGGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCCAGCCCCTACGGCGCGAACCAGGGGTGG
                                                                                                       GTGGCGTGGGACGCCAGGTGGCCAGGTACGCGCAGGACTACGCGGCGAAGCGCGCCGGG
 GCGGGGCGGCGTGGAGCGCCGCCGACGCGCTGCGGTCGTGGGACGAGAAGAGGAAC
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                                                                                                                                                                                                           Score 121.8; DB 1
Pred. No. 1.6e-13;
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; NAME/KEY: CDS
; LOCATION: (56)..(571)
US-10-068-347-3
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 258; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/068,347
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/267,052
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Simmons, Carl
APPLICANT: Acevedo, Pedro
APPLICANT: Crane, Virginia
TITLE OF INVENTION: Maize PR1 Polynucleotides
FILE REFERENCE: 35718/242798 (5718-151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 772
TYPE: DNA
ORGANISM: Zea
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                                                                                                                                                                                                                                                                                                                                                                  TACTAGCTAGCT
                             GCCGGCGTCTTCATCTGCAACTATTACCCGCCGGGCAACGTGATTGGACAGAGCCCT
                                             GGCGCCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGCCAGAGCCCCC
                                                                                    CAGGTGGTGTGGCGCAACACCGCCGAGGTCGGGTGCGCCC---AGGCCAGCTGCGCCACG
                                                                                                                                         TACAACCACGCCACCAACACCTGCTCCGCTCCGGCCAGTCGTGCGGCCACTACACG
                                                                                                                                                                                               GCGGGCTACGCCTGGACGCGTCGAACGCCGTGGGATCCTGGGCGGCGGAGAAGCAGTAC
                                                                                                                                                                                                                  GGCGACTGCCGGCTGCACTCCGGCGGGCCCTACGGGGAGAACCTGTTCTGGGGCTCG
                                                                                                                                                                                                                                                                                CAGGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCCAGCCCCTACGGCGCGCAACCAGGGGTGG
                                                                                                                                                                                                                                                                                                            GTGGCCTGGAACACCACGGTGG----CGGCGTACGCGCAGGCTACGCGAACCAGCGCGCG
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; ORGANISM: Oryza sativa
US-10-078-929-85
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Matches 270;
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LENGTH: 714
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio (
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PRIOR ETLING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-05-07
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NUMBER OF SEQ ID NOS: 208
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FILING DATE: 1999-05-11
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FILING DATE: 1999-05-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1999-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/133436
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             CGTCGGCCCGGTGAGCTGGGACCCCAAGGTCGCCAGCTTCGCGCAGAGCTACGCGGCCAA
                                                                                                                                                         CGTGGCCCCGCTGCGTGGAACGCGGGGCCTGGCTTCGGCGGCGCGCGGGGACGGTGGCGCA 367
                                                             GCGCGCCGGCGACTGCCGGCTGCAGCACTCCGGCGGGCCGTACGGCGAGAACATCTT---
                                                                                           GCAGCGGCGGCAGGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCAGCCCCTACGGCGCGAA 427
                                                                                                                                                                                           CCTCGCCGCCGTGCCCGTGGCCATCTCGCTGGCCATGGCGGCCACCACCACCACCTC
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Similarity 55.4%;
70; Conservative
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Odell, Joan
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Sakai, Hajime
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Thorpe, Catherine
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pred. No. 9.4e-13;
0; Mismatches 211;
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PRIOR FILING DATE: 1999-05-07
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PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133428
PRIOR APPLICATION NUMBER: 60/133428
PRIOR FILING DATE: 1999-05-11
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                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Office SEQ ID NO 99
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APPLICANT:
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CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
PRIOR FILING DATE: 2000-05-05
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/133436 PRIOR FILING DATE: 1999-05-11 PRIOR APPLICATION NUMBER: 60/137667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved TITLE OF INVENTION: Stress Response FILE REFERENCE: BB1357 US NA
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142
                              319 TGCGGTGGAACGCGGGCCTGGCTTCGGCGGCGGCGGCGGGACGGTGGCGCAGCAGCGGCGGC 378
                                                                                                 CCCCTAC
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Sakai, Hajime
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Thorpe, Catherine
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                                                                                                                                    Conservative
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                                                                                                                                                   12.1%; 56.9%;
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                                                                                                                                   Score 108.6; DB Pred. No. 3.4e-11 0; Mismatches 17
                                                                                                                                                                  DB 12;
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                                                                                                                                                                  Length
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Sequence 9, Application US/10068347
Patent No. US20020166146A1
GENERAL INFORMATION:
APPLICANT: Pioneer Hi-Bred International, Inc.
APPLICANT: Simmons, Carl
APPLICANT: Simmons, Carl
APPLICANT: Simmons, Pedro
APPLICANT: Crane, Virginia
TITLE OF INVENTION: Malze PR1 Polynucleotides and Methods of Use
FILE REFERENCE: 35718,2742798 (5718-151)
CURRENT APPLICATION NUMBER: US/10/068,347
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/267,052
PRIOR APPLICATION NUMBER: 00/267,052
PRIOR APPLICATION NUMBER: 00/267,052
PRIOR APPLICATION NUMBER: 00/267,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (1)..(285)
US-10-068-347-9
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Zea mays
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US-10-068-347-9
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
  671
                                                                                                                                   162 CCAGATCGTGTGGCGACGCACCACCGCCGTCGGCTGCGCCCGGGTGGCGTGCGACGGCGG
                                                                                                                                                                                                                           102 CGCCGACTACTCGTACGCCGACAACGCGTGCGCGCCAGGCCGGGAGTGCGCGCACTACAC
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CTAGCTAGCTGAGGTCATCAGGTCGTAGCGACGG
                                                                     CGCCACGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAAGGCCCAGAGCCCCTA 670
                                                                                                                                                             GCAGGTGGTGTGGCGCAACACCGCCGAGGTCGGGTGCGCCAGGCCAGGCCACGGG 610
                                                                                                                                                                                                                                                            GCGGTACACCCACGCCAACAACACGTGCGCCGGGGGGGGCAGTGCGGCACGTACAC 550
                                                                                                                                                                                                                                                                                                                     GGGCGGGCCGGCGTGGCGGCCCCGGGACGCCGTCGCGGACTGGGCCGCCGAGGG 101
                                          CGGGGTGTTCATCACCTGCAACTACTACCCGCCCGGCAACGTCGTCGGCGAGAGGCCGTA 281
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170; Conservative
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Pred. No. 5.1e-11;
0; Mismatches 104;
  704
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; LOCATION: (547)
US-10-078-929-97
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PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
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Best Local Similarity
Matches 228; Conserv
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TITLE OF INVENTION: Nucleic Acid Fragments
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
TITLE OF TRANSPORTED IN A TO THE TO THE TO THE TOTAL STREET TO THE TOTAL STR
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APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio
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CURRENT FILING DATE: 2002-02-19
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Thorpe, Catherine
Weng, Zude
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Odell, Joan T.
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FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
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PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133438
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US-10-078-929-83
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                                                                                                                                                                                NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office
SEQ ID NO 83
LENGTH: 534
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TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
                                      NAME/KEY: unsure LOCATION: (94)
NAME/KEY: unsure LOCATION: (178)
                                                                                                                      LENGTH: 534
TYPE: DNA
ORGANISM: Oryza :
FEATURE:
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PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/137667
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Thorpe, Catherine
Weng, Zude
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RESULT 13
US-10-068-347-1
US-10-068-347-1
; Sequence 1, Application US/10068347
; Patent No. US20020166146A1
; Patent No. US20020166146A1
APPLICANT: Pioneer Hi-Bred International, Inc.
APPLICANT: Simmons, Carl
APPLICANT: Acevedo, Pedro
APPLICANT: Crane, Virginia
TITLE OF INVENTION: Malie PRI Polynucleotides and
FILE REFERENCE: 35718,7242798 (5718-151)
CURRENT APPLICATION NUMBER: US/10/068,347
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/267,052
PRIOR FILING DATE: 2001-02-07
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 12 SOFTWARE: PatentIn version SEQ ID NO 1

3.0

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; TYPE: DNA; ORGANIE: Zea mays; FEATURE: ; PEATURE: ; NAME/KEY: CDS; LOCATION: (1)..(501) US-10-068-347-1
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US-09-938-842A-1676
                                                                                                      US-09-938-842A-1676
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Query
Best L
                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-66-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1676, Application Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 214; Conserv
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                          TYPE: DNA
ORGANISM: Arabidopsis
                                                                                                                                                                                                      LENGTH: 492
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; FEATURE:

NAME/KEY: misc_feature

; LOCATION: (1)...(152331)

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Best Local Similarity 47.7%;
Matches 215; Conservation
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SEQ ID NO 16
LENGTH: 152331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/095,407
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR FILING DATE: 1997-08-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 18
                                                                                                                                         22204
                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                GCGGTGGAACGCGGGCCTGGCTTCGGCGGCGCCGCGGGGACGGTGGCGCAGCAGCAGCGGCGGCA 379
                                                                                                      GCGGACGAGTACCTGGCGCCCACAACCAGGCGCGCGCGGCGGTGGGCGT-GGCCCCGCT 319
GAAACTCGGAGAGGTTGGGATGTGCAAAAGTGAGATGCAACAATGGTCAAACCTTTATCA
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Pred. No. 0.00079;
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Search completed: March 18, 2003, 16:30:06 Job time: 180 secs

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Perfect score:
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SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:
SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:
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SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:
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SIDS2/gcgdata/geneseq/geneseqn-emb1/NA20010.DAT:
SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:
SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ABA96418
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Maize PR1-C10 codi
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ALIGNMENTS

RESULT 1 ABA96417

ABA96417;

ABA96417 standard; cDNA; 898

ВP

Crane EH, 10-APR-2000; 2000US-195801P. 10-APR-2001; 2001US-0832320. CDS Maize; pathogen-related; PR1-C10; plant; transgenic; gene; ss. Maize PR1-C10 encoding cDNA SEQ ID NO 1 06-DEC-2001. US2001049834-A1. Zea mays (CRAN/) CRANE E H. (CRAN/) CRANE V C. 02-APR-2002 (first entry) Crane VC Location/Qualifiers 63..674 /product= "PR1-C10" /*tag=

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Best Local Simi
Matches 898;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 898 BP; 161 A; 295 C; 309 G; 133 T; 0 other;
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DB; AAM48742.
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TTTTGTGGTGTGATCCGGTGGTGTTCTTGGTGTTGTTGACAACTGCTTTGGTTTGGTGTA
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Pred. No. 2.5e-125;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid pathogen-related protein PRI-C10. The nucleic acid plants for enhanced disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-APR-2001; 2001US-0832320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding a pathogen-related protein isolated maize and designated PR1-C10, useful for transforming plants enhanced disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-APR-2000; 2000US-195801P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2001049834-A1
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 612 BP; 80 A; 231 C; 239 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 32; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CRAN/) CRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    781
                                                                              121
181
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                                                                                                                 183
                                                                                                                                                                                             123
                                                                                                                                                                                                                                                                                                                hes 612;
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DB; AAM48742.
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                                                                                                                                                      CGCGTCCTCATGCCGGGCGCGCGGGCGCGGTGACCAAGGCGCAGCAGGGTGGCACCGGC
                                                                                              CGCGTCCTCATGCCGGGCGCGCGGGCGGGGGGTGACCAAGGCGCAGCAGGAGGTGGCACCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EH,
pathogen-related;
                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease
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                                                                                                                                                                                                                                                                                                                Score 612; DB 24;
; Pred. No. 8.7e-83;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                62 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                       Length 612;
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This sequence represents the DNA sequence PR-1mz. This sequence was isolated by scr
                                    New DNA contg. plant systemic acquired resistance genes - and transgenic plants contg. them, impart disease and pest resistance, also Arabidopsis gene promoter to control DNA transcription
                          Claim
                                                                                             Alexander DC,
                                                                                                            (CIBA ) CIBA
                                                                                                                            13-JAN-1994;
                                                                                                                                          03-JAN-1995;
                                                                                                                                                                          W09519443-A2
                                                                                                                                                                                                                                       maize; PR-1;
                                                                                                                                                                                                                                               systemic
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                                                                                                                                                          20-JUL-1995
                                                                                                                                                                                                                                                                    PR-1 like gene PR-1mz
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                                                                       1995-263872/34.
DB; AAR91595.
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                                                                                                                                                                                                                                                                                                                                                                                                                           acco; protein-synthesis independent gene; cyclohexamide;
acquired reistance response; anti-pathogen; plant protection;
                        Page 70; 85pp;
                                                                                                            GEIGY AG
                                                                                                                                                                                                                                       SS.
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                            Ryals
                                                                                                                            94US-0181271
                                                                                                                                          95WO-IB00002
                                                                                                                                                                                               Location/Qualifiers 40..531
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                        English.
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screening
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maize PR-1 like
ng a BTH-induced
gene,
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RESULT 4
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Best Local S
Matches 259
                                                                    Key
                                                                                                                                               regulation; expression; disease resistance; genetic manipulation; tobacco mosaic virus; cucumber mosaic virus; ringspot virus; necrosis virus; maize dwarf virus; viroid; bacterial; insect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library of maize. The library was screened using a probe matching to the PR-1 barley clone HVPR1BR. This sequence, AAQ99800-Q99803 and AAQ99805 are all used in recombinant/chimaeric DNA molecules of the invention. These sequences were isolated by differential screening of cDNA library, followed by analysis by Northern hybridisation to RNA in the presence and absence of cyclohexamide. The genes are used in the creation of transgenic plants. All of these sequences confer anti-pathogenic properties to transgenic plants. Transgenic expression of 2 or more of the recombinant molecules of the invention that encode anti-pathogenic proteins provides a synergistic increase in plant protection, and may also offer protection against a wider range of
                                                                                                                                                                                                                            2ea
                                                                                                             Zea mays
                                                                                                                                        nematode;
                                                                                                                                                                                               Zea mays;
                                                                                                                                                                                                                                                       22-NOV-1999
                                                                                                                                                                                                                                                                                 AAZ21207;
                                                                                                                                                                                                                                                                                                              AAZ21207 standard;
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hes 259;
                                                                                                                                                                                                                       mays pathogenesis-related class I PR-1#83 gene.
                                                                                                                                                                                                                                                                                                                                                                                             CGCTCAGGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGCCCAGAGCCCCTACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGGCGCGACTCCACCGCCATCGGCTGTGCCCGCGTCGTCTGCGACAACAACGCCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCG---CCACGGGGGCGCA
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                                                                                                                                                                                            maize; pathogenesis-related class
                                                                                                                                      fungal; ss.
                                                                                                                                                                                                                                                    (first entry)
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                   /...ag= a
/product= "PR-1#83"
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                                                                   Location/Qualifiers
92..583
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                       "pathogenesis-related
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                                                                                                                                                                                            I; PR-1;
                       class
                                                                                                                                                                                            promoter;
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WO9943819-A1

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RESULT 5
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AC AAZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters isolated from a family of maize (Zea mays) genes encoding pathogenesis related (PR-1) proteins. The promoters are useful for expressing heterologous genes (Including genes for disease resistance) in plants, especially dicots, or monocots i.e. maize. The promoters are useful for the genetic manipulation of plants to exhibit specific phenotypes, particularly enhanced resistance to pathogen-caused disease. Pathogens include viruses such as tobacco or cucumber mosaic virus, ringspot virus, necrosis virus, and maize dwarf virus, and viroids, bacteria, insects, nematodes and fungi. The present sequence encodes a maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crane
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P-PSDB; AAY29944.
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27-MAR-1998;
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   22-NOV-1999
                           AAZ21191;
                                                    AAZ21191
                                                                                                                                                                                                                                                                    345
                                                                                                                                                                                                                                                                                                                                                                                             319
                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter sequences from pathogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein given in the present invention.
                                                                                                                  TCTTCATCATCTGCAGCTACAACCCGCCGGGCAACGTCGTCGGCGAGAGCCCCTACTAG
                                                                                                                                                                                TGTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCG----CCACGGGCGCCCA
                                                                                                                                                                                                                                  ACACCCACGCCAACAACACGTGCGCCGCGCGGCGCGCGGCACGTGCACGCAGGTGG
                                                                                                                                                                                                                                                                   CCGGCGCCGACTGGCGTCCGACGCCGTGGGCTCCTGGGTGTCCGAGAAGCAGTACT
                                                                                                                                                                                                                                                                                           GCGACTGCCAGCTGATCCACTCCGGCGGGCCCTACGGCGAGAACCTCTTCTGGGGCTCCG
                                                                                                                                                                                                                                                                                                                                            AGGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                  CGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGCCCAGAGCCCCTACTAG
                                                                                                                                                                  TGTGGCGCGACTCCACCGCCATCGGCTGTGCCCGGCGTCGTCTGCGACAACAACGCCGGCG
                                                                                                                                                                                                                   ACGACCACGACACCAGCTGCGCGGGGGGGGGGGGTGTGCGGCCACTACACGCAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Page 72-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      749
                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0076100
98US-0079648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US03011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 235 C; 206 G; 148 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                    ₽P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 139;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
1.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                          674
                                                                                                                                                                                           615
                                                                                                                                                                                                                                                                                               498
                                                                                                                                                                                                                                                                                                                                                                                                                                             318
                                                                                                                                                                   524
                                                                                                                                                                                                                     464
                                                                                                                                                                                                                                                                      404
                                                                                                                                                                                                                                                                                                                     344
                                                                                                                                                                                                                                                                                                                                              438
                                                                                                                                                                                                                                                                                                                                                                       284
                                                                                                                                                                                                                                                                                                                                                                                                                      227
                                                                                                                                                                                                                                             558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                               Qy
                                                              Qy
                                                                                         рь
                                                                                                               Qy
                                                                                                                                          Дb
                                                                                                                                                               Qy
                                                                                                                                                                                           Вр
                                                                                                                                                                                                                   Qy
                                         В
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                               AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters isolated from a family of maize (Zea mays) genes encoding pathogenesis related (PR-1) proteins. The promoters are useful for expressing heterologous genes (including genes for disease resistance) in plants, especially dicots, or monocots i.e. maize. The promoters are useful for the genetic manipulation of plants to exhibit specific phenotypes, particularly enhanced resistance to pathogen-caused disease. Pathogens include viruses such as tobacco or cucumber mosaic virus, incrosis virus, and maize dwarf virus, and viroids, bacteria, insects, nematodes and fungi. The present sequence encodes a maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nematode;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crane VC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-1998;
27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9943819-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 22; Page 65-66; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-SEP-1999
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PION-) PIONEER
                                                                                                                                                                                              145
                 496
                                                                                                                    379
                                                                                                                                                                   319
                                         325
                                                                  439
                                                                                           265
                                                                                                                                            205
                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mays
                                                                                                                                                                                              protein
                                                                                                                                          TGTCGTGGGATGAGAACGTGGCCGCCTTCGCGCGGAGCTACGCCGCAGCGCCAGGGCG
   GCGGCGGCAGCGCCTGGAAGGCGTCGGACGCCGTCGGCTTGTGGGGTGGGGGAGAAGCAGA
                                                     CGAGCTACCGCGC---GCGCCCCGCCGAGGTGGTGGCTGTGGGTGGCGGAGGGGCGGT
                                                                                           ACTGCAAGCTGGTGCACTCCGGCGGCGGGCCCAACCACTACGGGGAGAACATCTTCTGGG
                                                                                                                   AGGGCGGTGCGCGTTCGCGGACGTGGGGGCCCAGCCCCTACGGCGCGAACCAGGGGTGGG
                                                                                                                                                             TGCGGTGGAACGCGGGCCTGGCTTCGGCGGCGCCGCGGGACCGTGGCGCAGCAGCAGCGC
                                                                                                                                                                                                                                                                                                866
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                               BP;
                                                                                                                                                                                                                                                                                                                      given in the present invention.
                                                                                                                                                                                                                                                                                               213
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15.3%; A; 228 C;

Score 137.6; DB 20; Pred. No. 3e-12;

240 G; 185 T; 0 other;

0;

Mismatches

154;

Indels Length

7;

Gaps

Ψ

318

204

438

555 384 495 324 378

264

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Zea mays; maize; pathogenesis-related class I; PR-1; promoter; regulation; expression; disease resistance; genetic manipulation; tobacco mosaic virus; cucumber mosaic virus; ringspot virus; necrosis virus; maize dwarf virus; viroid; bacterial; insect;
New promoter sequences from pathogenesis-related genes
                                                                    1999-527621/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathogenesis-related
                                                                                                                                                                                                     98US-0076100
98US-0079648
                                                                                                                                                                                                                                                                         99WO-US03011
                                                                                                                                                           HI-BRED INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
111.581
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                        /note= "pathogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                                           /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                  "PR-1#52"
                                                                                                                                                             INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         class I PR-1#52
                                                                                                                                                                                                                                                                                                                                                                                                        class I protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
       of maize
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Ψ

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RESULT 6
AAZ21194
ID AAZ;
XX AAZ;
XX AAZ;
XX Zea
XX Zea
XX Zea
XX Zea
XX Cea
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                            AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters isolated from a family of maize (Zea mays) genes encoding pathogenesis related (PR-1) proteins. The promoters are useful for expressing heterologous genes (including genes for disease resistance) in plants, especially dicots, or monocots i.e. maize. The promoters are useful for the genetic manipulation of plants to exhibit specific phenotypes,
                                              particularly enhanced resistance to pathogen-caused disease. Pathoge include viruses such as tobacco or cucumber mosaic virus, ringspot virus, necrosis virus, and maize dwarf virus, and viroids, bacteria, insects, nematodes and fungi. The present sequence encodes a maize PR-1 protein given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crane
     Sequence 806
                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                           New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PION-) PIONEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1998;
27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nematode;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays; maize; pathogenesis-related class I; PR-1; promoter; regulation; expression; disease resistance; genetic manipulation; tobacco mosaic virus; coumber mosaic virus; ringspot virus; necrosis virus; maize dwarf virus; viroid; bacterial; insect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2ea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ21194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ21194 standard; DNA; 806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385
                                                                                                                                                                                                                                                                                                                                                                                                      promoter sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999-527621/44.
DB; AAY29943.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTGTGGCGCAACACCGCCGAGGTCGGGTGCGCGAGGCCAGCTGCGCCACGGGC---G
                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTACCT 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTAGCT 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGTCTTCATCACCTGCAACTACAACCCGCCGGGCAACTTCCGCGGACAGAGACCCTACT
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                                                                                                                                                                                                                                                                                                                                                       Page 74-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fungal; ss.
     B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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98US-0079648.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HI-BRED INT INC
  158 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "PR-1#93"
/note= "pathogenesi
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                                                                                                                                                                                                                                                                                                                                               86pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "pathogenesis-related
  243
  Ç
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                                                                                                                                                                                                                                                                                                                                                     English.
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260 G;
144 T;
1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                   maize
                                                                                                                                               Pathogens
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RESULT 7
ABL59008
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                      CDS
               New protein resistance 1
                                                                    (MITU ) MITSUBISHI CHEM CORP.
(BADA) BADAN PENGKAJIAN DAN PENERAPAN TEKNOLOGI (PAKR-) PT PAKRIE BROS.
(BIOI-) BIOINDUSTRY KYOKAI SH.
(DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
                                           P-PSDB;
                                                                                                                          20-SEP-2000; 2000JP-0285905
                                                                                                                                             20-SEP-2000;
                                                                                                                                                                02-APR-2002
                                                                                                                                                                                  JP2002095477-A.
                                                                                                                                                                                                                                              Elaeis guineensis
                                                                                                                                                                                                                                                               Antibacterial protein; microbe resistance;
                                                                                                                                                                                                                                                                                  Nucleotide sequence of an antibacterial protein.
                                                                                                                                                                                                                                                                                                      20-AUG-2002
                                                                                                                                                                                                                                                                                                                        ABL59008
                                                                                                                                                                                                                                                                                                                                          ABL59008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201
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DB; ABB77767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACCACCTGAGCAGCAACACCTGCGACCCCGGCAAGGTGTGCGGCCACTACACGCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACACCCACGCAACAACACGTGCGCCGCGGGGCGCAGTGCGGCACGTACACGCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGTCTTCATCGTCTGCAGCTACGACCCCCCGGGCAACGTCAACGGCCAGCGCCCGTTC
                                                                                                                                                                                                                                                                                                                                                                                                 CCACGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGCCAGAGCCCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                        GTGTGGCGCAGGTGTCCACCCGCATCGGCTGCGCGCGCGTCGTCTGCGCCGACAACCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGGCGGGTGCGCGTTCGCGGACGTGGGGGCCCAGCCCTACGGCGCGAACCAGGGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGCGTGGGACGCCAGGGTGGCCAGGTACGCGCAGGACTACGCGGCGAAGCGCGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCGGTGGAACGCGGGCCTGGCTTCGGCGGCGGCGGGGACGGTGGCGCAGCAGCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACTGCCGGCTGGTGCACTCGGGC----GGGCCGTTCGGCCAGAGCATCTTCTGGGGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254;
                                                                                                                                                                                                                                                                                                                                         standard; DNA; 846
              and its gene,
to pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                             2000JP-0285905
                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                           35..523
/*tag=
                                                                                                                                                                                                  /*tag= a
/product= "antibacterial
                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.6%;
                microbes
                         useful
                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 121.8; DI
Pred. No. 6.6e-
                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                       creating plants with
                                                                                                                                                                                                  protein"
                                                                                                                                                                                                                                                                plant;
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Claim 3;

Page 8-9; 13pp; Japanese

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RESULT 8
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ACC AAC4
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Best Local S
Matches 245
              25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a polypeptide which has antibacterial activity. The antibacterial protein and its polynucleotide can be used for the creation of a plant with resistance against pathogenic microbes
                                                                                                                                                                                                                                                                                        Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss
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                990S-0121825.
990S-0123180.
990S-0123548.
990S-01235788.
990S-0126264.
990S-0126785.
990S-0127462.
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56.1%;
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01-JUN-1999;
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RESULT 9
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Best Local Similarity 53.0%;
Matches 233; Conservative
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14-OCT 1999

21-OCT 1999

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                                             AAC37078;
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              (first entry)
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99US-0159329
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                                                                         DNA;
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Pred. No. 0.00019;
0; Mismatches 198;
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99US-014433.
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99US-0144632.
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19-JUL-1999
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9905-0139817.	9905-0139763.	99US-0139463.	99US-0139461. 99US-0139462.	99US-0139460.	99US-0139459.	9905-0139458.	9905-0139456.	9908-0139455.	99US-0139454.	99US-0139492.	9908-0139453.	9908-0139452.	9905-0139119.	99115-0138847	9905-0138540	9905-0139004	990S-0137373.	9908-0137528.	9905-0137222.	99US-0136782.	99US-0136392.	9908-0136021.	99US-0135629.	9905 0133124.	990S-0134941.	9905-0134941	9905-0134370.	9905-0134221.	99US-0134219.	99US-0134218.	990S-0134256.	9905-0132863.	9905-0132486.	99US-0132485.	99US-0132484.	9905-0132407.	9903-0131445.	99US-013U891.	9905-0130510.	99US-0130449.	9908-0130077.	9905-0120714.	9908-0120314	9908-0127462.	99US-0126785.	99US-0126264.	9905-0125788.	9908-0123548.	9903-0121023:	9975-0121825	2000EP-0301439.				thaliana.		assay; genetic mapping; gene expression control; ification; signal transduction pathway; hway; promoter; termination sequence; ss.		thaliana DNA fragment SEQ ID NO: 16099.
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444 AAACCTTTCTACAATTATAAGTCAGACACGTGTGCTGCGAACCACACGTGCGGGGTTTAT
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31-AUG-1999;
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         CGGCAGGGCGGTGCGCGTTCGCGGACGTGGGGGCCCAGCCCTACGGCGCGGAACCAGGGG
                                                                                                                 CCGCTGCGGTGGAACGCGGGCCTGGCTTCGGCGGCCGCGGGGACGGTGGCGCAGCAGCGG
                                                                                                                                  TGGGCGAGCTACCG-----CGCGCGCCCCCGCGAGGTGGTGGCGCTGTGGGTGGCGGAG
                                                                 AACCAAAAGAAGTGTGAGTTCGCGAGTCTAAACCCTGGAAAATACGGCGCGAACCAGCTT
                                                                                                 CCACTAGTTTGGAGCCAGACGTTGGAAGCTGCTGCGAGTCGGTTGGCTCGTTACCAGAGG
                                TGGGCTAAGGGCTTAGTAGCCGTGACACCGTCTCTTGCTGGAGACTTGGGTGAAGGAG
                                                                                                                                                                       232;
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                                                                                                                                                                   Score 83.6; DB 21;
Pred. No. 0.00032;
0; Mismatches 199;
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The specification describes antisense oligonucleotides (AAX52869-X55271) CC directed against at least 2 mRNAs selected from target genes, coding and conon-coding regions of RNAs corresponding to target genes, gene coding non-coding regions of RNAs corresponding to target genes, gene coding intron-exon borders, the comparison of the juxta-section between coding and non-coding cregions and all segments of RNAs encoding proteins associated with one cor more diseases, conditions or mixtures. The antisense oligonucleotides cor more diseases, conditions or mixtures. The antisense oligonucleotides corresponding proteins and conditions or mixtures. The antisense oligonucleotides coligonucleotides (specifically AAX55180-771) can be used for the coligonucleotides (specifically AAX55180-771) can be used for the conditions are those associated with impaired respiration and conditions are those associated with impaired respiration and confirmantion, allergic rhinitis, acute asthma, allergies, asthma, impeded crespiration, respiratory distress syndrome, pain, cystic fibrosis, constructive pulmonary disease (COPD), and cancers such as leukemias, and constructive pulmonary disease (COPD), and cancers such as leukemias, chronic constructive pulmonary disease (COPD), and cancers such as leukemias, chronic constructive pulmonary disease (COPD), and cancers such as leukemias, chronic constructive pulmonary disease (COPD), and cancers such as leukemias, chronic constructive pulmonary disease (COPD), and cancers such as leukemias, chronic constructive pulmonary disease (COPD).
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AAX53491/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcicolon cancer; breast cancer; lung cancer; pancreatic cancer; colon cancer; breast cancer; lung cancer; pancreatic cancer;
  lymphomas, carcinomas e.g. colon cancer, breast
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-229400/19
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17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                              vasoconstriction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 114955 BP;
                               acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
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   colon
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pulmonary vasoconstriction; inflammation; allergic rhinitis;
                                                                                                                                                                                                                                                                                                      Human adenosine Al receptor antisense oligonucleotide fragment.
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                                                                                                                                                                                                                                    Antisense oligonucleotide; multiple target; antisense
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   cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114955
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0.00027;
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                                                                                                                                                                                                                                           treatment;
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09-JUN-1998;
17-SEP-1997;
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                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                   prostate cancer;
                                                                                                                             New antisense oligonucleotides used vasoconstriction
                                                                                                                                             WPI; 1999-229400/19
                                                                                                                                                                                                                                       hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                    Disclosure;
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                                                                                                                                                                 EAST CAROLINA
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97US-0059160
                                                                                                                                                                                           98WO-US19419
                                                                                                                                    'n
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                                                                                                                                    of,
                                                                                                                                    O
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                                                                                                                                    pulmonary
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The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. golon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize Sequence 114955 BP; 6071 A; 29417 C; metastasized to the lungs, including breast and prostate cancer. 36712 G; 21328 т; Length 114955 21427 other;

밁 В 밁 Db Q 밁 Qy δÃ QΥ Qy Query Match Best Local Matches 104783 104723 104903 104843 104963 121181 301 241 Local Similarity hes 212; Conserv CGTGCTTGCTCCTCGCCACCCTCCTCGCGCTCTGCGCCGCCGGCGGCGGCCGACCCCACGGCG 180 BGGGCGCGSNNNDNNCCGCBGGCCBGGCGCSNNNDNNCCGCBGGCCBGGCGSNNNDNN 104782 GGGCGCGCCGGCCGGGCCGSNNNDNNGCBGGCCBGGGCGCGCCGGCCGGCCGG CGGTGGCCTGGCCTGCGGTGGAACGCGGGCCTGGCTTCGGCGGCGCCGCGGGACGG CCGCBGGCCBGNNNDNNCCGCBGGCCBNNNDNNCCGCBGGCCSNNNDNNCGCBGGCCB CCGCBGGCCBGGCSNNNDNNCCGCBGGCCBGGCSNNNDNNCCGCBGGCCBGGSNNNDNN 104842 CGCGCGTCCTCATGCCGGGCGCGCGGGCGCGCGGTGACCAAGGCGCAGCAGCAGCACCG NNNDNNCBGGCCBGGCGCCGCCGGCCGGGCCGSNNNDNNBGGCCBGGGCGCGCCCC -----TGGCGCAGCAGCGGCGGCAGGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCAGC Conservative 9.1%; 66; Score 81.6; DB 20; Pred. No. 0.00051; Mismatches 335; Indels 7; Gaps 413 104902 240 360 105022 104962 1;

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AACC AACC	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
RESULT 12 AAC47173 ID AAC47173; XX AC AAC47173; XX TO AAC47173; XX TO T18-OCT-2000 (first XX Hybridisation assay; XX Hybridisation assay; XX Hybridisation assay; XX Hybridisation assay; XX FOR Arabidopsis thaliana XX Hybridisation pathway; p XX FOR ARABIDOPSIS thaliana XX FOR ARABIDOPSIS thaliana XX FOR ARABIDOPSIS THALIANA XX FOR ARABIDOPSIS THALIANA XX FOR ARABIDOPSIS FOR OS-ARR-1999; 99US- PR OS-ARR-1998; 99US-	105023 GGCCGGG 474 CTGTGGG 105083 CGCCGCC 534 CAGTGCG 105143 GCGCGCC 594 GCCAGCT 105203 CGCCGCC 654 CAGGCCCG 105203 CGCCGCC 1 CGCCGCC 714 GCCCCGCC 714 GCCCCGCC
standard; DNA; 779 BP. 00 (first entry) is thaliana DNA fragment SEQ ID NO: 52827. tlon assay; genetic mapping; gene expression control; dentification; signal transduction pathway; pathway; promotef; termination sequence; ss. is thaliana. -A2. 00. 00. 2000EP-0301439. 99 99US-0121825. 99 99US-0125486. 99 99US-0120448. 99 99US-012448. 99 99US-012448. 99 99US-012448. 99 99US-012486. 99 99US-012426. 99 99 99 9US-012426. 99 99 90 90 90 90 90 90 90 90 90 90 90	GCCGGGCCGSNNNDNNGGCCGGGCGCGCGCCGGCCGGCCGGCCGGCCGGC
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       P-PSDB; ABB77766
                 WPI; 2002-439986/47.
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Local Similarity 50.6%;
hes 207; Conservative
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                                                                                                                                                                         japonica.
                                                                                                                                                                                                              sequence
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990S-0161360.
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990S-0161920.
990S-0161922.
990S-0161993.
990S-0162142.
                                                                                                                                                                                           protein; antibacterial agent; food;
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/product=
                                                                                                                                    Location/Qualifiers
34..522
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                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                              an antibacterial protein.
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                                                                                                                              "antibacterial protein"
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ismatches 193;
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99US-01510864
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99US-015108664
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99US-01510866

9905-015933 9905-015933 9905-0159638 9905-0159638 9905-0160767 9905-0160767 9905-0160767 9905-0160770 9905-0160814 9905-0160815 9905-0160981 9905-0160981 9905-0161404 9905-0161406

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          misc_feature
                                                                         misc_feature
                                                                                                 misc_feature
                                                                                                                                     Pseudorables virus; PRV; LLV; large latency attenuated virus; vaccine; early protein 0; protecting animals; deletion mutants; swine;
                           TATA_signal
                                                                                                                                                                    DNA encoding Pseudorabies virus large latency transcript
                                                                                                                         Pseudorabies virus
                                                                                                                                                                                       15-MAY-1995
                                                                                                                                                                                                                     AAQ73500 standard; DNA; 8438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes japonica. The protein can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibacterial protein gene of Wasabia japonica
                                                                                                                                                                                                                                                             470
                                                                                                                                                                                                                                                                                                                                                                245 GGCTCATACACTCTGGTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 AAGACTATCTAAGGGTTCACAACCAGGCACGAGCGGCGGTAGGCGTTGGCCCCATGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity es 216; Conserv
                                                                                                                                                                                                                                                                      GAAACTCGGTGAGACTCGGATGTGCTAAAGTGAGGTGTAACAATGGTGGAACGATCATCG
                                                                                                                                                                                                                                                                                                                                      ACGCCAACAACACGTGCGCCGCGGGGGGCGCAGGTGCGCACGTACACGCAGGTGGTGTGGC
                                                                                                                                                                                                                                                                                                                                                      GCGACTTATCTGGCATAAGCGCCGTGAACATGTGGGTTGACGAGAAGGCTGACTACAACT
                                                                                                                                                                                                                                                           TTTGCAACTATGATCCTCCTGGCAATTATGTGAACGAGAAGCCTTACAAATGAG
                                                                                                                                                                                                                                                                                                        GCAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCGCCACGGGCGCCACGCTCACGC
                                                                                                                                                                                                                                                                                                                        ACCCTTCGAACACGTGCAACGGAGTT-----TGTGGTCACTACACTCAGGTTGTTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                      GGTGCGCGTTCGCGGACGTGGGGGGCCAGCCCCTACGGCGCGAACCAGGGGGTGGGCCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                    GGGACGACAGGGTGGCAGCCTTCGCTCGGAGCTACGCAGACCAACTAAGAGGCGACTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      664 BP; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                       (first
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                                                                                      /*tag=
                           /note= "encodes
1..6
                                                 /note= "derived 622..6498
  /*tag=
                 /*tag=
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                                                                                /*tag= a
/note= "derived
                                                                                                       Location/Qualifiers
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                                           /*tag=
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52.2%;
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                  Ω
                                                                                                                                                                                                                                                                                                                                                                                      ------GTTCTTACGGCGAGAACTTGGCATGGGGAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; 165 G; 166 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71.2; DB Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an antibacterial protein of Wasabia used in an antibacterial agent and
                                predicted
                                                                                from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                         from
                                                         PRV strain
                                                                                PRV strain
                                                                                                                                       swine;
                                amino acid sequence of ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 24;
                                                                                                                                             transcript;
EPO; HSV-1 ICPO;
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AAQ73500 shows the Pseudorables virus (PRV) large latency transcript (CLIT). The basic sequence is derived from PRV strain InFh and PRV Strain Ka. The LIT overlaps and is transcribed in the opposite contentation with respect to the EPO (early polypeptide 0) and the CC immediately early gene (IE180). EPO is nonessential for replicatio, CC LLT is the only gene expressed during PRV latency, and the IE180 CC gene is absolutely necessary for PRV replication. However there are CC copies of IE180 in the genome. It is expected that PRV lacking one CC of the IE180 copies is viable. Deletions in the non-overlapping CC regions of these 3 genes will generate single deletion routants. CC while deletions in overlapping regions will generate double deletion comutants. The invention is concerned with the construction of attenuated cornuses which have a reduced ability to reactivate from latency. This CC can be achieved by functionally disabling the expression of the EPO CC gene, or by disrupting the synthesis of the LLT, or both. (See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New pseudorabies virus mutants for use in vaccine deletion and/or insertion in the early protein O g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCGCGTTCGCGGACGTGGGGGGCCAGCCCTACGGCGCGAACCAGGGGTGGGCGAGCTAC
                                                                                     GGGGCGCCCGCCGGCGGCGCGCGCGCGCGACGACGACGCCGGGCTGCTCGGGCCAG
                                                                                                                                                                                                                           GAGTACCTGGCGCGCACACCAGGCGCGCGCGCGGCGGTGGGCGTGGCCCCCGCTGCGGTGG
                                                                                                                                                                                                                                                                                                       GCGCGGTGACCAAGGCGCAGCAGGGTG-GCACCGGCAGCGAGGCAAGCGAACGCGAACGGCGAAC
                                                                                                                                                                                                                                                                                                                                                                                                         AGCGGCGCTTGCGCCGGGGCCCCCGGTCCTTCGTCGTCGCGGTGGCCGTGGCCGTCCC 4037
                                                                                                                                     AACGCGGGCCTGGCCTTCGGCGGCCGCCGGGGGACGGTGGCGCAGCAGCAGCGGCAGGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 70.4; DB 11,
Pred. No. 0.026;
""ematches 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 8438;
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RESULT 15
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                                                                                              This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-cp6-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two Cc classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of CC of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide CC types and for investigating cell differentiation of cell or tissue CC types and for investigating cell differentiation. The method allows the CC methylation status of many C residues to be determined simultaneously. CC abgl3410-Abg54121 represent genomic DNA sequences used to illustrate the cmethod for determining the degree of cytosine methylation described in the disconsure of the invention
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-371829/40
                                                                               disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGGCGCGGGCCCCGTCCACGCTGTAGCGCACCAGCGGCGCCCACGG 4499
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                                                                               invention
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                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                       GGCGCGGTGACCAAGGCGCAGCAGGGTGGCACCGGCAGCGACGGCGACGGCGAC
CGCGCGCGCCCGAGGTGGTGGCGCTGTGGGTGGCGGAGGGGGGGTACTACACCCAC
                                                                                                          TGCGCGTTCGCGGACGTGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGGGCGAGCTAC
                                                                                                                                 AACACCGCCGAGGTCGGGTGCGCGCAGGCCAGGCTGCGCCACGGGCGCCACGCTCACGCTC
                                            GCCAACAACACGTGCGCCGCGGGGGGCAGTGCGCACGTACACGCAGGTGGTGTGGCGC 566
                                                                                           CGCGGGCGGCGGTCGGCGGGGGGGCGCGGTNGCGGCGGCGGCGCGGAGCGGGCGNG
                               Conservative
                                                                                                                                                                                                                                                        7.8%;
                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                        Score 70;
Pred. No.
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                          0.034;
                                                                                                                                                                                                                                                              DB 24; Length 712;
                                                                                                                                                                                                                                                  252;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                        326
                                                                                                                                                                                                     266
                                                                                                                                                                                                                    290
                  626
                                                               588
                                                                              506
                                                                                             528
                                                                                                           446
                                                                                                                           468
                                                                                                                                          386
                                                                                                                                                        410
                                 648
```

Job time : 374 secs Search completed: March 18, 2003, 14:12:18